

## CONFIDENTIAL

## SEQUENCE LISTING

<110> Sleeman, Matthew  
Murison, Greg

<120> Fibroblast Growth Factor Receptors and Methods for Their Use

<130> 11000.1037c5

<150> U.S. 09/823,038  
<151> 2001-03-28

<150> U.S. 09/383,586  
<151> 1999-08-26

<150> U.S. 09/276,268  
<151> 1999-03-25

<150> PCT/NZ00/00015  
<151> 2000-02-18

<150> U.S. 60/221,216  
<151> 2000-07-25

<150> U.S. 10/157,444  
<151> 2000-05-28

<150> PCT/NZ03/00105  
<151> 2003-05-27

<160> 145

<170> FastSEQ for Windows Version 4.0

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<213> Mouse

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tgtgggtggc cagaagtttgc tgggtttgcc cacgggtat gtgtggcac ggcctgatgg 180  
ctcctacctc aacaagctgc tcatctctcg ggcccgccag gatgatgctg gcatgtacat 240  
ctgccttaggt gcaaatacca tgggctacag tttccgttagc gccttcctca ctgtattacc 300  
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ctgagccctg agtggcgtcc agtccagctc ccagtgaccg cgccctgtct tcaggtccga 180

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ctgaggcggc	gcgaggaccc	ccaagaatgg	cagacaaagt	ggtcccacgg	caggtggccc	300
gcctggccg	cactgtcg	ctacagtgcc	cagtggaggg	ggaccacca	ccgttgacca	360
tgtggaccaa	agatggccgc	acaatccaca	gtggctggag	ccgcttccgt	gtgctgcccc	420
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ccaatggctt	tggcagcctc	agcgtcaact	acactctcat	catcatggat	gatattagtc	540
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agaagtggac	actgagctt	aagaacctga	agcctgaaga	cagtggcaag	tacacgtgcc	840
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ggtagcgccg	ccccgcccag	gccgggcccgg	ggggcgccgg	gggcgggatg	cggcccccgg	180
ggcagcgatg	accgcgtcgc	gctgctcagg	ggcccggtc	tgaccccggt	gcctgctcgc	240
cgcggcccg	ctgatccctg	tcgagcgtct	acgcgcctcg	ttcccttgc	ctggagctcg	300
gcccggaggg	gggcccggacc	ctggctctgc	ggccgcgacc	tgggtttgc	gggcctgagc	360
cctgagtggc	gtccagtc	gctcccagt	accgcgcccc	tgcttcaggt	ccgaccggcg	420
agatgacgcg	gagccccgcg	ctgctgtgc	tgctattggg	ggccctcccg	tcggctgagg	480
cggcgcgaga	tgtatattgt	ccagggaaagg	agagccctgg	gccaggtgg	tcttcggggg	540
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aggctagtga	acacagaaaag	aagaagtgg	cactgagctt	gaagaacctg	aacccgtaaag	780
acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	gccacactaca	840
aagtggatgt	aatccagcgg	actcggttca	agcctgtgct	cacaggacaa	caccctgtga	900
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gcctgcatg	gcctgtggtg	atcggtatcc	cagctggtgc	tgttccatc	ctaggcactg	1320
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acacacatac acacacacctgc actcacacgc tctcatgtgg agggcaaggt tcatacacac	1620
cagcatgtcc actatcagtg ctaaatacag cgaatctcca agcactgtgt cctgaggtag	1680
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ag	1742

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<400> 4

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agatggcgga caaggtggtc ccacggcagg tggccggctg ggccgcactg tgcgctgca	180
gtgccagtgg agggggaccc gccgcccgt accatgtgga ccaaggatgg ccgcaccatc	240
cacagcggct ggagccgctt ccgcgtgctg ccgcaggggc tgaaggtgaa gcaggtggag	300
cgggaggatg cccgcgtgta cgtgtgcaag gccaccaacg gcttcggcag ccttagcgtc	360
aactacaccc tcgtcgtgct ggtgacatt agcccaggaa aggagagcct ggggcccac	420
agctcctctg ggggtcaaga ggaccccgcc agccagcagt gggcacgacc gcgcttcaca	480
cagccctcca agatgaggcg ccgggtgatc gcacggcccg tggtagctc cgtcggctc	540
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ttgacgcgcc cagaggccgc tgagccagg aagaagaagt ggacactgag cctgaagaac	660
ctgcggccgg aggacagcgg caaatacacc tgccgcgtgt cgaaccgcgc gggcccatc	720
aacgccacct acaagggtgga tgtgatccag cggaccgtt ccaagccgt gctcacaggc	780
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<213> Mouse

<220>  
<221> VARIANT  
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<223> Xaa = Any Amino Acid

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Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu	
20 25 30	
Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val	
35 40 45	
Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn	
50 55 60	
Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile	
65 70 75 80	
Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu	
85 90 95	
Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser	
100 105 110	
Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Xaa Gly Ile Pro	
115 120 125	

<210> 6  
<211> 529  
<212> PRT  
<213> Mouse

<400> 6

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Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro  
 1 5 10 15  
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val  
 20 25 30  
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro  
 35 40 45  
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg  
 50 55 60  
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu  
 65 70 75 80  
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys  
 85 90 95  
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile  
 100 105 110  
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser  
 115 120 125  
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg  
 130 135 140  
 Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val  
 145 150 155 160  
 Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro  
 165 170 175  
 Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala  
 180 185 190  
 Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys  
 195 200 205  
 Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly  
 210 215 220  
 Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser  
 225 230 235 240  
 Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe  
 245 250 255  
 Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro  
 260 265 270  
 Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His  
 275 280 285  
 Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr  
 290 295 300  
 Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu  
 305 310 315 320  
 Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly  
 325 330 335  
 Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu  
 340 345 350  
 Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser  
 355 360 365  
 Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val  
 370 375 380  
 Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys  
 385 390 395 400  
 Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro  
 405 410 415  
 Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala  
 420 425 430  
 Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile  
 435 440 445  
 Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr  
 450 455 460  
 Thr Asp Val His Thr His Thr His Thr His Cys Thr His Thr Leu  
 465 470 475 480  
 Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val  
 485 490 495  
 Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp

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Gly	Pro	Arg	500	Gln	Gln	Val	Gly	Arg	505	Ile	Glu	Asn	Asn	Gly	510	
			515						520					Gly	Arg	Val
Ser																

<210> 7  
 <211> 439  
 <212> PRT  
 <213> Mouse

<400> 7  
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 20 25 30  
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln  
 35 40 45  
 Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val  
 50 55 60  
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser  
 65 70 75 80  
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu  
 85 90 95  
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser  
 100 105 110  
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val  
 115 120 125  
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile  
 130 135 140  
 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn  
 145 150 155 160  
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg  
 165 170 175  
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly  
 180 185 190  
 Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gln Lys Phe  
 195 200 205  
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr  
 210 215 220  
 Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met  
 225 230 235 240  
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala  
 245 250 255  
 Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Pro Gly Pro Pro Met  
 260 265 270  
 Ala Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly  
 275 280 285  
 Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu  
 290 295 300  
 Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val  
 305 310 315 320  
 Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys  
 325 330 335  
 Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala  
 340 345 350  
 Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys  
 355 360 365  
 Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His  
 370 375 380  
 Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro  
 385 390 395 400  
 Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys

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405	410	415
Pro Glu Val Gly Ile Trp Gly Pro Arg	Gln Gln Val Gly Arg	Ile Glu
420	425	430
Asn Asn Gly Gly Arg Val Ser		
435		

<210> 8  
<211> 322  
<212> PRT  
<213> Mouse

<400> 8

Arg Arg Ala Pro Cys Cys Ser Cys Cys Arg Arg Cys Cys Trp Gly	1	5	10	15
Pro Ser His Arg Pro Pro Pro Glu Ala Pro Gln Arg Trp Arg Thr	20	25	30	
Arg Trp Ser His Gly Arg Trp Pro Ala Gly Pro His Cys Ala Ala Ala	35	40	45	
Val Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp	50	55	60	
Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln	65	70	75	80
Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val Tyr Val	85	90	95	
Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu	100	105	110	
Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp	115	120	125	
Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg	130	135	140	
Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg	145	150	155	160
Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro	165	170	175	
Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro	180	185	190	
Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn	195	200	205	
Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg	210	215	220	
Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr	225	230	235	240
Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val	245	250	255	
Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val	260	265	270	
Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly	275	280	285	
Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu	290	295	300	
Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys	305	310	315	320
Pro Leu				

<210> 9  
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<212> DNA  
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agcttgaaga acctgaagcc tgaagacagt ggcaagtaca cgtgccgtgt atctaacaag	180

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gcggactcgt	tccaaagcctg	tgctcacagg	gacacaccct	gtgaacacaa	cggtgactt	360
cggtgggaca	acgtcccttc	agtgcaggt	gcfgcgtgac	gtgaaggctg	tgatccagt	420
gctgaagcgg	gtggagtagc	gctccgaggg	acgcccacaac	tccaccattg	atgtgggtgg	480
ccagaagttt	gtgggtgtgc	ccacgggtga	tgtgtggtca	cggcctgtat	gctccctacct	540
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gtgtatcgcc	atcccagctg	gtgctgtctt	catccttaggc	actgtgctgc	tctggcttt	1020
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&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Mouse

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&lt;400&gt; 11

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37

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&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 12

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18

&lt;210&gt; 13

&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 13

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro  
1 5 10 15Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val  
20 25 30Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro  
35 40 45Val Glu Gly Asp Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg  
50 55 60Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu  
65 70 75 80

Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys

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	85	90	95												
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
				100		105							110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
				115		120						125			
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
				130		135					140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
				145		150				155				160	
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
				165		170				170			175		
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
				180		185				185			190		
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
				195		200				200		205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
				210		215				220					
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser
				225		230				235			240		
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe
				245		250				250			255		
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro
				260		265				265		270			
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His
				275		280				280		285			
Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr
				290		295				295		300			
Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu
				305		310				315			320		
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly
				325		330				330			335		
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu
				340		345				345		350			
Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser
				355		360				360		365			
Thr	Ser	Leu	Pro	Trp											
				370											

&lt;210&gt; 14

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 14

Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val
1			5					10					15		
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys
				20		25				25			30		
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala
				35		40				40		45			
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys
				50		55				55		60			
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His
				65		70				70		75		80	
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro
				85		90				90		95			
Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys
				100		105				105		110			
Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu
				115		120				120		125			
Asn	Asn	Gly	Gly	Arg	Val	Ser									
				130		135									

## CONFIDENTIAL

<210> 15  
 <211> 37  
 <212> PRT  
 <213> Mouse

<400> 15

Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val  
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 Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg  
 20 25 30  
 Pro Asp Gly Ser Tyr  
 35

4

<210> 16  
 <211> 1515  
 <212> DNA  
 <213> Human

<400> 16

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccaagtgg	agggggaccc	gccggccgtg	180
accatgttga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgtcg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agctcctctg	ggggtaaga	ggaccccgcc	420
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gcacggcccg	tgggtagctc	cgtcggctc	aagtgcgtgg	ccagcgggca	ccctcgccccc	540
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cactatcagt	gcttag					1515

<210> 17  
 <211> 504  
 <212> PRT  
 <213> Human

<400> 17

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
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 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala  
 20 25 30  
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg  
 35 40 45  
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr  
 50 55 60  
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu  
 65 70 75 80

## CONFIDENTIAL

Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val  
 85 90 95  
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr  
 100 105 110  
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly  
 115 120 125  
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp  
 130 135 140  
 Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile  
 145 150 155 160  
 Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly  
 165 170 175  
 His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr  
 180 185 190  
 Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Trp Thr Leu Ser Leu  
 195 200 205  
 Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser  
 210 215 220  
 Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln  
 225 230 235 240  
 Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr  
 245 250 255  
 Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser  
 260 265 270  
 Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala  
 275 280 285  
 Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gln Lys Phe Val  
 290 295 300  
 Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu  
 305 310 315 320  
 Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr  
 325 330 335  
 Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe  
 340 345 350  
 Leu Thr Val Leu Pro Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser  
 355 360 365  
 Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro  
 370 375 380  
 Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln  
 385 390 395 400  
 Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly  
 405 410 415  
 His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu  
 420 425 430  
 Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu  
 435 440 445  
 Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro  
 450 455 460  
 Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr  
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 His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val  
 485 490 495  
 His Gln His Ile His Tyr Gln Cys  
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<210> 18  
 <211> 1161  
 <212> DNA  
 <213> Human

<400> 18  
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60  
120

## CONFIDENTIAL

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gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggccgg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgccatc	aacgccacct	acaaggtgga	tgtatccac	720
ccaaaaccgc	aagggccacc	tgtggctcc	tcgtcctcg	ccactagcct	gccgtggccc	780
gtggtcatcg	gcatcccagc	cggcgtgtc	ttcatcctgg	gcaccctgct	cctgtggctt	840
tgccaggccc	agaagaagcc	gtgcacccccc	gcccctgccc	ctcccctgcc	tgggcaccgc	900
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&lt;210&gt; 19

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 19

Met	Thr	Pro	Ser	Pro	Leu	Pro	Pro	Leu	Leu	Leu	Leu						
1					5				10						15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala		
					20				25				30				
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg		
					35				40			45					
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr		
					50				55			60					
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu		
					65				70			75			80		
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val		
					85				90			95					
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr		
					100				105			110					
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly		
					115				120			125					
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp		
					130				135			140					
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile		
					145				150			155			160		
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly		
					165				170			175					
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr		
					180				185			190					
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu		
					195				200			205					
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser		
					210				215			220					
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	His		
					225				230			235			240		
Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser		
					245				250			255					
Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile		
					260				265			270					
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys		
					275				280			285					
Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr		
					290				295			300					

## CONFIDENTIAL

Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu  
 305 310 315 320  
 Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala  
 325 330 335  
 Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu  
 340 345 350  
 Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Ser  
 355 360 365  
 His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His Tyr  
 370 375 380  
 Gln Cys  
 385

<210> 20  
 <211> 1230  
 <212> DNA  
 <213> Human

<400> 20

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<210> 21  
 <211> 409  
 <212> PRT  
 <213> Human

<400> 21

Met	Thr	Pro	Ser	Pro	Leu						
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Arg	Gly	Pro	Pro
				20			25			30	
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly
							35			40	
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr
							50			55	
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg
							65			70	
Pro	Gln	Gly	Leu	Lys	Val	Gln	Val	Glu	Arg	Glu	Asp
							85			90	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu
							100			105	
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys
							115			120	
											125

## CONFIDENTIAL

Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp  
 130 135 140  
 Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn  
 145 150 155 160  
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg  
 165 170 175  
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly  
 180 185 190  
 Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe  
 195 200 205  
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr  
 210 215 220  
 Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met  
 225 230 235 240  
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala  
 245 250 255  
 Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Gln Gly Pro Pro Val Ala  
 260 265 270  
 Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile  
 275 280 285  
 Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys  
 290 295 300  
 Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro  
 305 310 315 320  
 Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp  
 325 330 335  
 Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys  
 340 345 350  
 Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly  
 355 360 365  
 Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His  
 370 375 380  
 Thr His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys  
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 Val His Gln His Ile His Tyr Gln Cys  
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<210> 22  
 <211> 1434  
 <212> DNA  
 <213> Human

<400> 22

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## CONFIDENTIAL

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<210> 23  
<211> 477  
<212> PRT  
<213> Human

<400> 23					
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20	25	30			
Asp Lys Val Val Pro Arg Gln Val Ala Arg	Leu	Gly	Arg	Thr	Val
35	40	45			
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro	Leu	Thr	Met	Trp	Thr
50	55	60			
Lys Asp Gly Arg Thr Ile His Ser Gly Trp	Ser	Arg	Phe	Arg	Val
65	70	75	80		
Pro Gln Gly Leu Lys Val Lys Gln Val	Glu	Arg	Glu	Asp	Ala
85	90	95			
Tyr Val Cys Lys Ala Thr Asn Gly Phe	Gly	Ser	Leu	Ser	Val
100	105	110			
Thr Leu Val Val Leu Ala Arg Pro Arg	Phe	Thr	Gln	Pro	Ser
115	120	125			Lys
Arg Arg Arg Val Ile Ala Arg Pro Val	Gly	Ser	Ser	Val	Arg
130	135	140			Leu
Cys Val Ala Ser Gly His Pro Arg Pro	Asp	Ile	Thr	Trp	Met
145	150	155			Lys
Asp Gln Ala Leu Thr Arg Pro Glu Ala	Ala	Glu	Pro	Arg	Lys
165	170	175			
Trp Thr Leu Ser Leu Lys Asn Leu	Arg	Pro	Glu	Asp	Ser
180	185	190			Gly
Thr Cys Arg Val Ser Asn Arg Ala	Gly	Ala	Ile	Asn	Ala
195	200	205			Thr
Val Asp Val Ile Gln Arg Thr Arg Ser	Lys	Pro	Val	Leu	Gly
210	215	220			Thr
His Pro Val Asn Thr Thr Val Asp Phe	Gly	Gly	Thr	Thr	Ser
225	230	235			Phe
Cys Lys Val Arg Ser Asp Val Lys Pro	Val	Ile	Gln	Trp	Leu
245	250	255			Lys
Val Glu Tyr Gly Ala Glu Gly Arg His	Asn	Ser	Thr	Ile	Asp
260	265	270			Val
Gly Gln Lys Phe Val Val Leu Pro	Thr	Gly	Asp	Val	Gly
275	280	285			
Asp Gly Ser Tyr Leu Asn Lys Leu	Leu	Ile	Thr	Arg	Ala
290	295	300			Arg
Asp Ala Gly Met Tyr Ile Cys Leu	Gly	Asn	Thr	Met	Gly
305	310	315			Tyr
Phe Arg Ser Ala Phe Leu Thr Val	Leu	Pro	Asp	Pro	Lys
325	330	335			Pro
Pro Pro Val Ala Ser Ser Ser Ala	Thr	Ser	Leu	Pro	Trp
340	345	350			Pro
Val Ile Gly Ile Pro Ala Gly Ala	Val	Phe	Ile	Leu	Val
355	360	365			
Leu Trp Leu Cys Gln Ala Gln	Lys	Pro	Cys	Thr	
370	375	380			
Pro Pro Leu Pro Gly His Arg Pro	Pro	Gly	Thr	Ala	Arg
385	390	395			Asp
Gly Asp Lys Asp Leu Pro Ser Leu	Ala	Ala	Leu	Ser	Arg
405	410	415			

## CONFIDENTIAL

Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu  
 420 425 430  
 Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr  
 435 440 445  
 Thr Asp Ile His Thr His Thr His Ser His Thr His Ser His  
 450 455 460  
 Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys  
 465 470 475

<210> 24  
 <211> 1242  
 <212> DNA  
 <213> Human

&lt;400&gt; 24

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ccggccgccc	ccgccccaga	tgacattagc	ccagggaaagg	agagcctggg	gcccacacgc	120
tcctctgggg	gtcaagagga	ccccggccagc	cagcagtggg	cacgaccgc	cttcacacag	180
ccctccaaga	tgaggcgccg	ggtgatcgca	cggccctgg	gtagctccgt	gcggctcaag	240
tgcgtggcca	gcgggcaccc	tcggcccgac	atcacgtgga	tgaaggacga	ccaggccttg	300
acgcgcccag	aggccgctga	gcccaggaag	aagaagtgg	cactgagcct	gaagaacctg	360
cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcg	accgcgcggg	cgccatcaac	420
gccacactaca	aggtggatgt	gatccagcgg	accgcgttcca	agcccgtgt	cacaggcacg	480
caccccgta	acacgacggt	ggacttcggg	gggaccacgt	ccttcagtg	caaggtgcgc	540
agcgacgtga	agccggtgat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	gggcggccag	aagttgtgg	tgctgcccac	gggtgacgtg	660
tggtcgccc	ccgacggctc	ctaccta	aagctgctca	tcaccctgtc	ccgcccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
tccctcaccg	tgctgccaga	cccaaaaccg	caagggccac	ctgtggcctc	ctcgccctcg	840
gccactagcc	tgccgtggcc	cgtggtcatc	ggcatcccag	ccggcgctgt	cttcatcctg	900
ggcacccctgc	tcctgtggct	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgcctgccc	960
cctccctgc	ctgggcacccg	cccgcgggg	acggcccg	accgcagcgg	agacaaggac	1020
cttccctcgt	tggccccc	cagcgctggc	cctgggtgtgg	ggctgtgtga	ggagcatggg	1080
tctccggcag	ccccccagca	tttactgggc	ccagggccag	ttgctggccc	taagttgtac	1140
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	1200
gtggaggcga	aggccacca	gcacatccac	tatcagtgt	ag		1242

<210> 25  
 <211> 413  
 <212> PRT  
 <213> Human

&lt;400&gt; 25

Met	Thr	Pro	Ser	Pro	Leu										
1				5			10			15					
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
				20			25			30					
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
				35			40			45					
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
				50			55			60					
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
				65			70			75			80		
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
				85			90			95					
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
				100			105			110					
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
				115			120			125					
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
				130			135			140					
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr
				145			150			155			160		

## CONFIDENTIAL

His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln  
 165 170 175  
 Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg  
 180 185 190  
 Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly  
 195 200 205  
 Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro  
 210 215 220  
 Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp  
 225 230 235 240  
 Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser  
 245 250 255  
 Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Gln Gly  
 260 265 270  
 Pro Pro Val Ala Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val  
 275 280 285  
 Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu  
 290 295 300  
 Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala  
 305 310 315 320  
 Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser  
 325 330 335  
 Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly  
 340 345 350  
 Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu  
 355 360 365  
 Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr  
 370 375 380  
 Thr Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser His  
 385 390 395 400  
 Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys  
 405 410

&lt;210&gt; 26

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 26

atgacgcccga	gccccctgtt	gctgctcctg	ctggccgcgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgcccagg	ccccccaaag	atggccgaca	agggtggtccc	acggcaggtg	120
gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgttgg	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agctcctctg	ggggtaaga	ggaccccgcc	420
agccagcagt	gggacccaaa	accgcaagg	ccacctgtgg	cctcctcg	ctcgccact	480
agcctgcccgt	ggcccgttgt	catcgccatc	ccagccggcg	ctgtcttcat	cctggcacc	540
ctgctcctgt	ggcttgcca	ggcccagaag	aagccgtgca	cccccgcc	tgccctccc	600
ctgcctgggc	accgcccggc	ggggacggcc	cgccgaccgca	gcggagacaa	ggacccccc	660
tcgttggccg	ccctcagcgc	tggcccttgt	gtggggctgt	gtgaggagca	tgggtctccg	720
gcagcccccc	agcacttact	gggcccaggc	ccagttgctg	gccctaagtt	gtacccaaa	780
ctctacacag	acatccacac	acacacacac	acacactctc	acacacactc	acacgtggag	840
ggcaagggtcc	accagcacat	ccactatcag	tgctag			876

&lt;210&gt; 27

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 27

Met Thr Pro Ser Pro Leu Leu Leu Leu	Leu Leu Pro Pro Leu Leu	Leu	Leu
1	5	10	15

## CONFIDENTIAL

Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala  
 20 25 30  
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg  
 35 40 45  
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Leu Thr Met Trp Thr  
 50 55 60  
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu  
 65 70 75 80  
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val  
 85 90 95  
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr  
 100 105 110  
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly  
 115 120 125  
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp  
 130 135 140  
 Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser Ser Ala Thr  
 145 150 155 160  
 Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe  
 165 170 175  
 Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro  
 180 185 190  
 Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly  
 195 200 205  
 Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala  
 210 215 220  
 Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro  
 225 230 235 240  
 Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys  
 245 250 255  
 Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His  
 260 265 270  
 Ser His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His  
 275 280 285  
 Tyr Gln Cys  
 290

<210> 28  
 <211> 1080  
 <212> DNA  
 <213> Human

<400> 28

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ccggccgccc	ccgcccgggg	ccccccaaag	atggcggaca	agggtggtccc	acggcaggtg	120
ccccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccggccgctg	180
accatgttga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggcacgaccg	360
cgcttcacac	agccctccaa	gatgaggcgc	cggtgatcg	cacggcccg	ggtagctcc	420
gtgcggctca	agtgcgtggc	cagcgggcac	cctcggcccg	acatcacgtg	gatgaaggac	480
gaccaggcct	tgacgcgccc	agaggccgct	gagcccagga	agaagaagtg	gacactgagc	540
ctgaagaacc	tgcggccgga	ggacagcggc	aaatacacct	gccgcgtgtc	gaaccgcgcg	600
ggcgccatca	acgcccaccta	caaggtggat	gtgatccacc	caaaccgc	agggccacct	660
gtggcctcct	cgtcctcgcc	cactagcctg	ccgtggcccg	tggtcatcg	catcccagcc	720
ggcgctgtct	tcatcctggg	caccctgctc	ctgtggcttt	gccaggccca	gaagaagccg	780
tgcacccccc	cgcctgcccc	tcccctgcct	gggcaccgc	cgccggggac	ggcccgac	840
cgcagcggag	acaaggacct	tccctcggt	gccgcctca	gcgctggccc	tggtgtgggg	900
ctgtgtgagg	agcatgggtc	tccggcagcc	ccccagcact	tactggccc	aggcccagtt	960
gctggcccta	agttgtaccc	caaactctac	acagacatcc	acacacacac	acacacacac	1020
tctcacacac	actcacacgt	ggagggcaag	gtccaccagc	acatccacta	tcagtgttag	1080

<210> 29

## CONFIDENTIAL

<211> 359  
 <212> PRT  
 <213> Human

&lt;400&gt; 29

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala  
 20 25 30  
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg  
 35 40 45  
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr  
 50 55 60  
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu  
 65 70 75 80  
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val  
 85 90 95  
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr  
 100 105 110  
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met  
 115 120 125  
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys  
 130 135 140  
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp  
 145 150 155 160  
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys  
 165 170 175  
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr  
 180 185 190  
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys  
 195 200 205  
 Val Asp Val Ile His Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser  
 210 215 220  
 Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala  
 225 230 235 240  
 Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala  
 245 250 255  
 Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His  
 260 265 270  
 Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro  
 275 280 285  
 Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu  
 290 295 300  
 His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val  
 305 310 315 320  
 Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His  
 325 330 335  
 Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val His  
 340 345 350  
 Gln His Ile His Tyr Gln Cys  
 355

<210> 30  
 <211> 1149  
 <212> DNA  
 <213> Human

&lt;400&gt; 30

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ccggccgccc	ccgcccagg	ccccccaaag	atggcggaca	aggtggtccc	acggcaggtg	120
gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300

## CONFIDENTIAL

gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggagcggacc	360
cgttccaagc	ccgtgctcac	aggcacgcac	cccgtgaaca	cgacggtgga	tttcgggggg	420
accacgtcct	tccagtgcaa	ggtgcgcagc	gacgtgaagc	cggtgatcca	gtggctgaag	480
cgcgtggagt	acggcgcgcg	gggcccacac	aactccacca	tcgatgtggg	cggccagaag	540
tttgtggtgc	tgcccacggg	tgacgtgtgg	tcgcggccc	acggctccta	cctcaataag	600
ctgctcatca	cccgtgccc	ccaggacgat	gcgggcatgt	acatctgcct	tggcgcacac	660
accatgggct	acagctccg	cagcgccttc	ctcaccgtgc	tgccagaccc	aaaaccgcaa	720
gggcccacctg	tggcctcctc	gtcctcggcc	actagcctgc	cgtggccgt	ggtcatcgcc	780
atcccagccg	gcgctgtctt	catcctggc	accctgctcc	tgtggctttg	ccaggcccag	840
aagaagccgt	gcaccccccgc	gcctgcccct	cccctgcctg	ggcaccgccc	gccggggacg	900
gcccgcgacc	gcagcggaga	caaggacctt	ccctcggtgg	ccgcccctcag	cgctggccct	960
ggtgtgggc	tgtgtgagga	gcatgggtct	ccggcagccc	cccagcactt	actgggccc	1020
ggcccagttg	ctggccctaa	gttgtacccc	aaactctaca	cagacatcca	cacacacaca	1080
cacacacact	ctcacacaca	ctcacacgtg	gagggcaagg	tccaccagca	catccactat	1140
cagtgttag						1149

&lt;210&gt; 31

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 31

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	1
					5				10						15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala	20
									25						30	
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	35
								40				45				
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	50
								55			60					
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	65
									70		75				80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val	85
								90							95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	100
								105							110	
Thr	Leu	Val	Val	Leu	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	115
								120							125	
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	130
								135			140					
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	145
								150			155				160	
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	165
								170							175	
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	180
								185							190	
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	195
								200			205					
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	210
								215							220	
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	225
								230			235				240	
Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro		245
									250						255	
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	260
									265			270				
Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	275
								280				285				
Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	290
								295			300					
Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	305
									310		315				320	
Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	

## CONFIDENTIAL

325	330	335
Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu		
340	345	350
Tyr Thr Asp Ile His Thr His Thr His Ser His Thr His Ser		
355	360	365
His Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys		
370	375	380

&lt;210&gt; 32

&lt;211&gt; 888

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 32

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tcctctgggg	gtcaagagga	ccccgcccagc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgaggcgccg	ggtgatcgca	cggccctgtgg	gtagctccgt	gcggctcaag	240
tgcgtggcca	gcgggcaccc	tcggcccgac	atcacgtgga	tgaaggacga	ccaggccttg	300
acgcgcccag	aggccgctga	gcccaggaag	aagaagtgg	cactgagcct	gaagaacctg	360
cggccggagg	acagcgccaa	atacaccctgc	cgcgtgtcg	accgcgcggg	cgccatcaac	420
gccacctaca	aggtggatgt	gatccaccca	aaaccgcaag	ggccacactgt	ggcctcctcg	480
tcctcggcca	ctagcctgcc	gtggccctgt	gtcatcgca	tcccagccgg	cgctgtcttc	540
atcctgggca	ccctgctcct	gtggctttgc	caggcccaga	agaagccgtg	caccccccgcg	600
cctgcccctc	ccctgcctgg	gcaccgcccc	ccggggacgg	cccgcgaccg	cagcggagac	660
aaggaccttc	cctcggtggc	cgccctcagc	gctggccctg	gtgtggggct	gtgtgaggag	720
catgggtctc	cggcagcccc	ccagcactta	ctggggccag	gcccaattgc	tggccctaag	780
ttgtacccca	aactctacac	agacatccac	acacacacac	acacacactc	tcacacacac	840
tcacacgtgg	aggcaggt	ccaccagcac	atccactatc	agtgttag		888

&lt;210&gt; 33

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 33

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu						
1	5	10	15			
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly						
20	25	30				
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro						
35	40	45				
Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met						
50	55	60				
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys						
65	70	75	80			
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp						
85	90	95				
Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys						
100	105	110				
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr						
115	120	125				
Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys						
130	135	140				
Val Asp Val Ile His Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser						
145	150	155	160			
Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala						
165	170	175				
Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala						
180	185	190				
Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His						
195	200	205				
Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro						

## CONFIDENTIAL

210	215	220													
Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu
225					230				235					240	
His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
					245				250					255	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His
					260				265					270	
Thr	His	Thr	His	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His	
					275				280					285	
Gln	His	Ile	His	Tyr	Gln	Cys									
					290				295						

&lt;210&gt; 34

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 34

atgacgccga	gccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgcccggaga	tgacattagc	ccagggagg	agagcctggg	gcccacagc	120
tcctctgggg	gtcaagagga	ccccgcccagc	cagcagtggg	agcggacccg	ttccaagccc	180
gtgctcacag	gcacgcaccc	cgtgaacacg	acgggtggact	tcggggggac	cacgtccttc	240
cagtgcagg	tgcgcagcga	cgtgaagccg	gtgatccagt	ggctgaagcg	cgtggagtac	300
ggcgccgagg	gccgccacaa	ctccaccatc	gatgtggcg	gccagaagtt	tgtggtgctg	360
cccacgggtg	acgtgtggtc	gcggcccgac	ggctcctacc	tcaataagct	gctcatcacc	420
cgtgcccggcc	aggacgatgc	gggcatgtac	atctgccttg	gcccacaacac	catgggctac	480
agcttccgca	gccccttcct	caccgtgctg	ccagacccaa	aaccgcaagg	gccacctgtg	540
gcctcctcg	cctcggccac	tagcctgccc	tggcccgtgg	tcatcgcat	cccagccggc	600
gctgtcttca	tcctgggcac	cctgctcctg	tggcttgcc	aggcccagaa	gaagccgtgc	660
accccccgcgc	ctgcccctcc	cctgcctggg	caccggccgc	cggggacggc	ccgcgaccgc	720
agcggagaca	aggaccttcc	ctcggtggcc	gccctcagcg	ctggccctgg	tgtgggctg	780
tgtgaggagc	atgggtctcc	ggcagcccc	cagcacttac	tgggcccagg	cccagttgct	840
ggccctaagt	tgtacccaa	actctacaca	gacatccaca	cacacacaca	cacacactct	900
cacacacact	cacacgtgga	gggcaaggtc	caccagcaca	tccactatca	gtgcttag	957

&lt;210&gt; 35

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 35

Met	Thr	Pro	Ser	Pro	Leu	Pro	Pro	Leu	Leu	Leu						
1				5				10			15					
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	
					20				25			30				
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	
					35				40			45				
Ala	Ser	Gln	Gln	Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	
					50				55			60				
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	
					65				70			75			80	
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	
					85				90			95				
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	
					100				105			110				
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	
					115				120			125				
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	
					130				135			140				
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	
					145				150			155			160	
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	
					165				170			175				

## CONFIDENTIAL

Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro  
 180 185 190  
 Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu  
 195 200 205  
 Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro  
 210 215 220  
 Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg  
 225 230 235 240  
 Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro  
 245 250 255  
 Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His  
 260 265 270  
 Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu  
 275 280 285  
 Tyr Thr Asp Ile His Thr His Thr His Ser His Thr His Ser  
 290 295 300  
 His Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys  
 305 310 315

<210> 36  
 <211> 1161  
 <212> DNA  
 <213> Human

<400> 36

atgacgccga	gccccctgtt	gctgctcctg	ctgcccgcgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgcccggac	acgaccgcgc	ttcacacagc	cctccaagat	gaggcgccgg	120
gtgatcgac	ggcccgtggg	tagctccgtg	cggctcaagt	gcgtggccag	cgggcaccct	180
cggcccgaca	tcacgtggat	gaaggacgac	caggcctga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacctacaa	ggtggatgtg	360
atccagcgga	cccgttccaa	gcccgtgctc	acaggcacgc	accccgtgaa	cacgacggtg	420
gacttcgggg	ggaccacgtc	tttccagtgc	aaggtgcgca	gcgacgtgaa	gccggtgatc	480
cagtggctga	agcgcgtgga	gtacggcgcc	gagggccgcc	acaactccac	catcgatgtg	540
ggcggccaga	agtttgtggt	gctgcccacg	ggtgacgtgt	ggtcgccgccc	cgacggctcc	600
tacctaata	agctgctcat	cacccgtgcc	cgccaggacg	atgcgggcat	gtacatctgc	660
cttggcgcca	acaccatggg	ctacagcttc	cgcagcgcct	tcctcaccgt	gctgccagac	720
ccaaaaccgc	aagggccacc	tgtggcctcc	tcgtcctcg	ccactagcct	gccgtggccc	780
gtggtcatcg	gcatcccagc	cggcgctgtc	ttcatctgg	gcaccctgct	cctgtggctt	840
tgccaggccc	agaagaagcc	gtgcacccccc	gcgcctgccc	ctcccctgcc	tgggcaccgc	900
ccgcccggga	cggcccgca	ccgcagcgga	gacaaggacc	ttcccctcg	ggccgcccctc	960
agcgctggcc	ctggtgtggg	gctgtgtgag	gagcatgggt	ctccggcagc	cccccagcac	1020
ttactgggcc	caggcccagt	tgctggccct	aagttgtacc	ccaaactcta	cacagacatc	1080
cacacacaca	cacacacaca	ctctcacaca	cactcacacg	tggagggcaa	ggtccaccag	1140
cacatccact	atcagtgcta	g				1161

<210> 37  
 <211> 386  
 <212> PRT  
 <213> Human

<400> 37

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr  
 20 25 30  
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser  
 35 40 45  
 Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile  
 50 55 60  
 Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu  
 65 70 75 80  
 Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu

## CONFIDENTIAL

85	90	95
Asp Ser Gly Lys Tyr Thr Cys Arg Val	Ser Asn Arg Ala Gly	Ala Ile
100	105	110
Asn Ala Thr Tyr Lys Val Asp Val	Ile Gln Arg Thr Arg	Ser Lys Pro
115	120	125
Val Leu Thr Gly Thr His Pro Val	Asn Thr Thr Val Asp	Phe Gly Gly
130	135	140
Thr Thr Ser Phe Gln Cys Lys Val	Arg Ser Asp Val Lys	Pro Val Ile
145	150	155
Gln Trp Leu Lys Arg Val Glu Tyr	Gly Ala Glu Gly	Arg His Asn Ser
165	170	175
Thr Ile Asp Val Gly Gly Gln Lys	Phe Val Val Leu Pro	Thr Gly Asp
180	185	190
Val Trp Ser Arg Pro Asp Gly Ser	Tyr Leu Asn Lys	Leu Leu Ile Thr
195	200	205
Arg Ala Arg Gln Asp Asp Ala	Gly Met Tyr Ile Cys	Leu Gly Ala Asn
210	215	220
Thr Met Gly Tyr Ser Phe Arg Ser	Ala Phe Leu Thr Val	Leu Pro Asp
225	230	235
Pro Lys Pro Gln Gly Pro Pro Val	Ala Ser Ser Ser	Ala Thr Ser
245	250	255
Leu Pro Trp Pro Val Val Ile Gly	Ile Pro Ala Gly Ala	Val Phe Ile
260	265	270
Leu Gly Thr Leu Leu Leu Trp	Leu Cys Gln Ala Gln	Lys Lys Pro Cys
275	280	285
Thr Pro Ala Pro Ala Pro Pro	Leu Pro Gly His Arg	Pro Pro Gly Thr
290	295	300
Ala Arg Asp Arg Ser Gly Asp Lys	Asp Leu Pro Ser	Leu Ala Ala Leu
305	310	315
Ser Ala Gly Pro Gly Val Gly	Leu Cys Glu Glu His	Gly Ser Pro Ala
325	330	335
Ala Pro Gln His Leu Leu Gly Pro	Gly Pro Val Ala Gly	Pro Lys Leu
340	345	350
Tyr Pro Lys Leu Tyr Thr Asp Ile	His Thr His Thr His	Thr His Ser
355	360	365
His Thr His Ser His Val Glu	Gly Lys Val His Gln	His Ile His Tyr
370	375	380
Gln Cys		
385		

&lt;210&gt; 38

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 38

atgacgcccga	gccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgccccagg	ccccccaaag	atggccgaca	agggtggtccc	acggcagggtg	120
gccccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggacccaaaa	360
ccgcaagggc	cacctgtggc	ctcctcgtcc	tcggccacta	gcctgccgtg	gcccgtggtc	420
atcggcatcc	cagccggcgc	tgtcttcatc	ctgggcaccc	tgctcctgtg	gctttgcccag	480
gcccgagaaga	agccgtgcac	ccccgcgcct	gcccctcccc	tgcctgggca	ccgcccggccg	540
gggacggccc	gcgaccgcag	cggagacaag	gacctccct	cggtggccgc	cctcagcgct	600
ggccctggtg	tggggctgtg	tgaggagcat	gggtctccgg	cagcccccca	gcacttactg	660
ggcccaggcc	cagttgtgg	ccctaagttq	taccccaaac	tctacacaga	catccacaca	720
cacacacaca	cacactctca	cacacactca	cacgtggagg	gcaagggtcca	ccagcacatc	780
cactatcagt	gctag					795

&lt;210&gt; 39

&lt;211&gt; 264

## CONFIDENTIAL

<212> PRT  
 <213> Human

&lt;400&gt; 39

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala  
 20 25 30  
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg  
 35 40 45  
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr  
 50 55 60  
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu  
 65 70 75 80  
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val  
 85 90 95  
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr  
 100 105 110  
 Thr Leu Val Val Leu Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser  
 115 120 125  
 Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro  
 130 135 140  
 Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln  
 145 150 155 160  
 Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly  
 165 170 175  
 His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu  
 180 185 190  
 Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu  
 195 200 205  
 Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro  
 210 215 220  
 Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr  
 225 230 235 240  
 His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val  
 245 250 255  
 His Gln His Ile His Tyr Gln Cys  
 260

&lt;210&gt; 40

<211> 603  
 <212> DNA  
 <213> Human

&lt;400&gt; 40

atgacgcccga	ccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgccccaga	tgacattagc	ccagggagg	agagcctggg	gcccgcacagc	120
tcctctgggg	gtcaagagga	ccccgcccagc	cagcagtggg	acccaaaacc	gcaaggggcca	180
cctgtggcct	cctcgccctc	ggccacttagc	ctgcccgtggc	ccgtggcat	cgccatccca	240
gccggcgctg	tcttcatcct	gggcaccctg	ctcctgtggc	tttgccaggc	ccagaagaag	300
ccgtgcaccc	ccgcgcctgc	ccctccctg	cctgggcacc	gcccggccgg	gacggcccgc	360
gaccgcagcg	gagacaagga	ccttccctcg	ttggccgccc	tcagcgctgg	ccctgggtgtg	420
gggctgtgtg	aggagcatgg	gtctccggca	gccccccagc	acttactggg	cccaggccca	480
gttgctggcc	ctaagttgta	ccccaaactc	tacacagaca	tccacacaca	cacacacaca	540
cactctcaca	cacactcaca	cgtggagggc	aaggtccacc	agcacatcca	ctatcagtgc	600
tag						603

&lt;210&gt; 41

<211> 200  
 <212> PRT  
 <213> Human

&lt;400&gt; 41

## CONFIDENTIAL

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly  
 20 25 30  
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro  
 35 40 45  
 Ala Ser Gln Gln Trp Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser  
 50 55 60  
 Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro  
 65 70 75 80  
 Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln  
 85 90 95  
 Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly  
 100 105 110  
 His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu  
 115 120 125  
 Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu  
 130 135 140  
 Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro  
 145 150 155 160  
 Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr  
 165 170 175  
 His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val  
 180 185 190  
 His Gln His Ile His Tyr Gln Cys 200  
 195

&lt;210&gt; 42

&lt;211&gt; 807

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 42

atgacgcccga	gccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgccccgagc	acgaccgcgc	ttcacacagc	cctccaagat	gaggcgccgg	120
gtgatcgac	ggcccgtggg	tagctccgtg	cggctcaagt	gcgtggccag	cgggcaccct	180
cggcccgaca	tcacgtggat	gaaggacgac	caggcattga	cgcgcccaga	ggccgcttag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacq	ccacccataaa	ggtggatgtg	360
atccacccaa	aaccgcaagg	gccacctgtg	gcctcctcg	cctcgccac	tagcctgccc	420
tggcccggtgg	tcatcgccat	cccagccggc	gctgtttca	tcctgggcac	cctgctcctg	480
tggctttgcc	aggcccagaa	gaagccgtgc	accccccgc	ctgcccctcc	cctgcctggg	540
caccgcccgc	cggggacggc	ccgcgaccgc	agcggagaca	aggaccttcc	ctcggtggcc	600
gccctcagcg	ctggccctgg	tgtggggctg	tgtgaggagc	atgggtctcc	ggcagcccc	660
cagcacttac	tgggcccagg	cccagttgct	ggccctaagt	tgtaccccaa	actctacaca	720
gacatccaca	cacacacaca	cacacactct	cacacacact	cacacgtgga	ggcaaggtc	780
caccagcaca	tccactatca	gtgctag				807

&lt;210&gt; 43

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 43

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr  
 20 25 30  
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser  
 35 40 45  
 Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile  
 50 55 60  
 Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu

## CONFIDENTIAL

65	70	75	80
Pro Arg Lys Lys Lys Trp Thr Leu Ser		Leu Lys Asn Leu Arg Pro Glu	
85		90	95
Asp Ser Gly Lys Tyr Thr Cys Arg Val		Ser Asn Arg Ala Gly Ala Ile	
100	105	110	
Asn Ala Thr Tyr Lys Val Asp Val		Ile His Pro Lys Pro Gln Gly Pro	
115	120	125	
Pro Val Ala Ser Ser Ser Ala Thr Ser		Leu Pro Trp Pro Val Val	
130	135	140	
Ile Gly Ile Pro Ala Gly Ala Val Phe	Ile	Leu Gly Thr Leu Leu	
145	150	155	160
Trp Leu Cys Gln Ala Gln Lys Lys Pro		Cys Thr Pro Ala Pro Ala Pro	
165		170	175
Pro Leu Pro Gly His Arg Pro Pro Gly		Thr Ala Arg Asp Arg Ser Gly	
180	185	190	
Asp Lys Asp Leu Pro Ser Leu Ala Ala		Gly Pro Gly Val	
195	200	205	
Gly Leu Cys Glu Glu His Gly Ser Pro	Ala	Pro Gln His Leu Leu	
210	215	220	
Gly Pro Gly Pro Val Ala Gly Pro Lys	Leu	Tyr Pro Lys Leu Tyr Thr	
225	230	235	240
Asp Ile His Thr His Thr His Ser His	Thr	His Ser His Val	
245	250	255	
Glu Gly Lys Val His Gln His Ile His	Tyr	Gln Cys	
260	265		

&lt;210&gt; 44

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 44

atgacgccga	gccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgcg	ccgcccaga	gcggaccgt	tccaagccg	tgctcacagg	cacgcacccc	120
gtgaacacga	cggtgactt	cgggggacc	acgtccttcc	agtgcaggt	gcgcagcgac	180
gtgaagccgg	tgatccagtg	gctgaagcgc	gtggagtagc	gcccgcagg	ccgcccacaac	240
tccaccatcg	atgtggcgg	ccagaagttt	gtggtgctgc	ccacgggtga	cgtgtggtcg	300
cggcccgacg	gctcctacct	caataagctg	ctcatcaccc	gtgcccgc	ggacgatgcg	360
ggcatgtaca	tctgccttgg	cgcacacacc	atgggctaca	gcttccgcag	cgccttcctc	420
accgtgtgc	cagacccaaa	accgcaaggg	ccacctgtgg	cctccctcg	ctcgccact	480
agcctgccgt	ggcccgtgt	catcgcatc	ccagccggcg	ctgttcat	cctgggcacc	540
ctgctctgt	ggcttgcca	ggcccagaag	aagccgtgca	cccccgcc	tgcccctccc	600
ctgcctggc	accgcccgc	ggggacggcc	cgcgaccgca	gcggagacaa	ggaccttccc	660
tcgttggccg	ccctcagcgc	tggccctgg	gtggggctgt	gtgaggagca	tgggtctccg	720
gcagcccccc	agcacttact	gggcccaggc	ccagttgctg	gccctaagtt	gtaccccaa	780
ctctacacag	acatccacac	acacacacac	acacactctc	acacacactc	acacgtggag	840
ggcaaggatcc	accagcacat	ccactatcg	tgctag			876

&lt;210&gt; 45

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 45

Met Thr Pro Ser Pro Leu Leu Leu Leu		Leu Pro Pro Leu Leu	
1	5	10	15
Gly Ala Phe Pro Pro Ala Ala Ala		Ala Arg Glu Arg Thr Arg	Ser Lys
20		25	30
Pro Val Leu Thr Gly Thr His Pro	Val	Asn Thr Thr Val	Asp Phe Gly
35		40	45
Gly Thr Thr Ser Phe Gln Cys Lys	Val	Arg Ser Asp Val	Lys Pro val
50		55	60
Ile Gln Trp Leu Lys Arg Val Glu	Tyr	Gly Ala Glu	Gly Arg His Asn

## CONFIDENTIAL

65	70	75	80
Ser Thr Ile Asp Val Gly Gly Gln Lys	Phe Val Val Leu Pro Thr Gly		
85	90	95	
Asp Val Trp Ser Arg Pro Asp Gly	Ser Tyr Leu Asn Lys	Leu	Leu Ile
100	105	110	
Thr Arg Ala Arg Gln Asp Asp Ala	Gly Met Tyr Ile Cys	Leu	Gly Ala
115	120	125	
Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe	Leu Thr Val Leu Pro		
130	135	140	
Asp Pro Lys Pro Gln Gly	Pro Pro Val Ala Ser	Ser Ser Ala	Thr
145	150	155	160
Ser Leu Pro Trp Pro Val Val Ile Gly	Ile Pro Ala Gly Ala Val	Phe	
165	170	175	
Ile Leu Gly Thr Leu Leu Leu Trp	Leu Cys Gln Ala Gln	Lys Lys Pro	
180	185	190	
Cys Thr Pro Ala Pro Ala Pro Pro	Leu Pro Gly His Arg	Pro Pro Gly	
195	200	205	
Thr Ala Arg Asp Arg Ser Gly	Asp Lys Asp Leu Pro	Ser Leu Ala Ala	
210	215	220	
Leu Ser Ala Gly Pro Gly Val Gly	Leu Cys Glu Glu His	Gly Ser Pro	
225	230	235	240
Ala Ala Pro Gln His Leu Leu Gly	Pro Gly Pro Val Ala Gly	Pro Lys	
245	250	255	
Leu Tyr Pro Lys Leu Tyr Thr Asp	Ile His Thr His Thr	His Thr His	
260	265	270	
Ser His Thr His Ser His Val Glu	Gly Lys Val His Gln	His Ile His	
275	280	285	
Tyr Gln Cys			
290			

&lt;210&gt; 46

&lt;211&gt; 522

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 46

atgacgccga	gccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgcccgaga	cccaaaacccg	caaggccac	ctgtggcctc	ctcgccctcg	120
gccactagcc	tgccgtggcc	cgtggtcattc	ggcatcccg	ccggcgctgt	tttcattcctg	180
ggcacccctgc	tcctgtggct	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgcctgcc	240
cctcccccgc	ctgggcacccg	ccgcgggggg	acggcccg	accgcagcgg	agacaaggac	300
cttccctcgt	tggccgcct	cagcgctggc	cctgggtgtgg	ggctgtgtga	ggagcatggg	360
tctccggcag	ccccccagca	cttactggc	ccaggccccag	ttgctggccc	taagttgtac	420
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	480
gtggagggca	aggccacca	gcacatccac	tatcagtgt	ag		522

&lt;210&gt; 47

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 47

Met Thr Pro Ser Pro Leu Leu Leu	Leu Leu Pro Pro Leu Leu		
1	5	10	15
Gly Ala Phe Pro Pro Ala Ala Ala	Arg Asp Pro Lys Pro Gln Gly		
20	25	30	
Pro Pro Val Ala Ser Ser Ser Ala	Thr Ser Leu Pro Trp Pro Val		
35	40	45	
Val Ile Gly Ile Pro Ala Gly	Ala Val Phe Ile Leu Gly Thr	Leu Leu	
50	55	60	
Leu Trp Leu Cys Gln Ala Gln	Lys Pro Cys Thr Pro Ala Pro Ala		
65	70	75	80
Pro Pro Leu Pro Gly His Arg	Pro Pro Gly Thr Ala Arg Asp Arg	Ser	

## CONFIDENTIAL

	85	90	95												
Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly
				100			105						110		
val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu
				115			120					125			
Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
				130			135			140					
Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His
				145			150			155			160		
Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys			
				165			170								

<210> 48  
<211> 1072  
<212> DNA  
<213> Human

<400> 48

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ccccggctgg	gccgcactgt	gccccgtcag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgt	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agctccctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccg	tggtagctc	cgtcggctc	aagtgcgtgg	ccagcgggca	ccctcggccc	540
gacatcacgt	gatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggccgg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgcacatc	aacgcacact	acaaggtgga	tgtgatccag	720
cggacccgtt	ccaagcccgt	gctcacaggc	acgcaccccg	tgaacacgac	ggtggacttc	780
ggggggacca	cgtccttcca	gtgcaaggtg	cgcagcgacg	tgaagccggt	gatccagtgg	840
ctgaagcgcg	tggagtacgg	cgccgagggc	cgccacaact	ccaccatcga	tgtggcggc	900
cagaagtttgc	tggtgctgcc	cacgggtgac	gtgtggtcgc	ggcccacgg	ctcctacctc	960
aataagctgc	tcatcacccg	tgcccggccag	gacgatgcgg	gcatgtacat	ctgccttggc	1020
gccaacacca	tgggctacag	cttccgcagc	gccttcctca	ccgtgctgcc	ag	1072

<210> 49  
<211> 357  
<212> PRT  
<213> Human

<400> 49

Met	Thr	Pro	Ser	Pro	Leu	Pro	Pro	Leu	Leu	Leu						
1				5			10			15						
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala	
					20			25			30					
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	
					35			40			45					
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	
					50			55			60					
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	
					65			70			75			80		
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val	
					85			90			95					
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	
					100			105			110					
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	
					115			120			125					
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	
					130			135			140					
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Arg	Val	Ile
					145			150			155			160		

## CONFIDENTIAL

Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly  
 165 170 175  
 His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr  
 180 185 190  
 Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu  
 195 200 205  
 Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser  
 210 215 220  
 Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln  
 225 230 235 240  
 Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr  
 245 250 255  
 Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser  
 260 265 270  
 Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala  
 275 280 285  
 Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val  
 290 295 300  
 Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu  
 305 310 315 320  
 Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr  
 325 330 335  
 Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe  
 340 345 350  
 Leu Thr Val Leu Pro  
 355

&lt;210&gt; 50

&lt;211&gt; 718

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 50

atgacgcccga	gccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgcccagg	ccccccaaag	atggccgaca	agggtggccc	acggcagggt	120
gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccggcgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agctcctctg	ggggtaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccg	tggtagctc	cgtgcggctc	aagtgcgtgg	ccagcggca	ccctcggccc	540
gacatcacgt	gatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggccgg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgcacatc	aacgcccac	acaaggtgga	tgtgatcc	718

&lt;210&gt; 51

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 51

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu						
1	5	10	15			
Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala						
20	25	30				
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg						
35	40	45				
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr						
50	55	60				
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu						
65	70	75	80			
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val						

## CONFIDENTIAL

	85		90		95										
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
			115				120				125				
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
					130		135			140					
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile
					145		150		155			160			
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly
					165			170			175				
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr
					180			185			190				
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu
					195			200			205				
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser
					210		215			220					
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	
					225		230			235					

&lt;210&gt; 52

&lt;211&gt; 787

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 52

atgacgcccga	gccccctgtt	gctgctcctg	ctgcccgcgc	tgctgctggg	ggcccttccca	60
ccggccgccc	ccgccccgagg	cccccccaaag	atggcggaca	aggtggtccc	acggcagggtg	120
ccccggctgg	gccgcactgt	gccccgtcag	tgcccagtgg	agggggaccc	gccggccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agctcctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggagccggac	ccgttccaag	cccgtgctca	caggcacgca	ccccgtgaac	480
acgacggtgg	acttcggggg	gaccacgtcc	ttccagtgca	aggtgcgcag	cgacgtgaag	540
ccgggtatcc	agtggctgaa	gcgcggtggag	tacggcgccg	agggccgcca	caactccacc	600
atcgatgtgg	gcggccagaa	gtttgtggtg	ctgcccacgg	gtgacgtgtg	gtcgcggccc	660
gacggctcct	acctaataa	gctgctcatc	acccgtgccc	gccaggacga	tgcgggcatg	720
tacatctgcc	ttggcgccaa	caccatgggc	tacagcttcc	gcagcgcctt	cctcaccgtg	780
ctgcccag						787

&lt;210&gt; 53

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 53

Met	Thr	Pro	Ser	Pro	Leu	Pro	Pro	Leu	Leu	Leu						
1				5				10				15				
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala	
					20			25				30				
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	
					35			40			45					
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr		
					50			55			60					
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	
					65			70			75			80		
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val	
					85			90			95					
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	
					100			105			110					
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	
					115			120			125					

## CONFIDENTIAL

Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp  
 130 135 140  
 Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn  
 145 150 155 160  
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg  
 165 170 175  
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly  
 180 185 190  
 Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe  
 195 200 205  
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr  
 210 215 220  
 Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met  
 225 230 235 240  
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala  
 245 250 255  
 Phe Leu Thr Val Leu Pro  
 260

&lt;210&gt; 54

&lt;211&gt; 991

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 54

atgacgccga	gccccctgtt	gctgctcctg	ctgcccgc	tgctgctggg	ggccttccca	60
ccggccgc	ccgcccagg	ccccccaaag	atggccgaca	aggtgtccc	acggcagggt	120
ccccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgcccctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggcacgaccg	360
cgcttcacac	agccctccaa	gatgaggcgc	cgggtgatcg	cacggcccgt	ggtagctcc	420
gtgcggctca	agtgcgtggc	cagcgggcac	cctcggcccg	acatcacgtg	gatgaaggac	480
gaccaggcct	tgacgcgccc	agaggccgct	gagcccagga	agaagaagtg	gacactgagc	540
ctgaagaacc	tgcggccgga	ggacagcggc	aaatacacct	gccgcgtgtc	gaaccgcgcg	600
ggcgccatca	acgcccaccta	caaggtggat	gtgatccagc	ggaccgttc	caagccgtg	660
ctcacaggca	cgcacccgt	gaacacgacg	gtggacttcg	gggggaccac	gtccttccag	720
tgcaagggtgc	gcagcgtacgt	gaagccggtg	atccagtggc	tgaagcgcgt	ggagtagcggc	780
gccgaggggcc	gccacacaactc	caccatcgat	gtggcggcc	agaagttgt	ggtgctgccc	840
acgggtgacg	tgtggtcgcg	gcccgacggc	tcctaccta	ataagctgt	catcacccgt	900
gcccggccagg	acgatgcggg	catgtacatc	tgccttggcg	ccaacaccat	gggctacagc	960
ttccgcagcg	cttcctcac	cgtgctgcca	g			991

&lt;210&gt; 55

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 55

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu						
1	5	10	15			
Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala						
20	25	30				
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg						
35	40	45				
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Leu Thr Met Trp Thr						
50	55	60				
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu						
65	70	75	80			
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val						
85	90	95				
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr						
100	105	110				

## CONFIDENTIAL

Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met  
 115 120 125  
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys  
 130 135 140  
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp  
 145 150 155 160  
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys  
 165 170 175  
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr  
 180 185 190  
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys  
 195 200 205  
 Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr  
 210 215 220  
 His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln  
 225 230 235 240  
 Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg  
 245 250 255  
 Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly  
 260 265 270  
 Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro  
 275 280 285  
 Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp  
 290 295 300  
 Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser  
 305 310 315 320  
 Phe Arg Ser Ala Phe Leu Thr Val Leu Pro  
 325 330

&lt;210&gt; 56

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 56

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgaggcgc	ggtgatcgca	cggccctgtgg	gtagctccgt	gcggctcaag	240
tgctgtggcca	gcgggcaccc	tcggcccac	atcacgtgga	tgaaggacga	ccaggccttg	300
acgcgcccag	aggccgctga	gcccaggaag	aagaagtgg	cactgagcct	gaagaacctg	360
cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcga	accgcgcggg	cgcacatcaac	420
gccacactaca	agggtggatgt	gatccagcg	acccgttcca	agcccgtgt	cacaggcacg	480
caccccgta	acacgacggt	ggacttcggg	gggaccacgt	ccttccagtg	caaggtgcgc	540
agcgacgtga	agccgggtat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	gggcggccag	aagttgtgg	tgctgcccac	gggtgacgtg	660
ttgttcgcggc	ccgacggtc	ctaccta	aagctgctca	tcacccgtgc	ccgcccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgcccag					799

&lt;210&gt; 57

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 57

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu	Pro Pro Leu Leu					
1 5 10 15						
Gly Ala Phe Pro Pro Ala Ala Ala	Arg Asp Asp Ile Ser Pro Gly					
20 25 30						
Lys Glu Ser Leu Gly Pro Asp Ser Ser	Gly Gly Gln Glu Asp Pro					
35 40 45						
Ala Ser Gln Gln Trp Ala Arg Pro Arg	Phe Thr Gln Pro Ser Lys Met					

## CONFIDENTIAL

50	55	60	
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys			
65	70	75	
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp		80	
85	90	95	
Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys			
100	105	110	
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr			
115	120	125	
Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys			
130	135	140	
Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr			
145	150	155	160
His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln			
165	170	175	
Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg			
180	185	190	
Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly			
195	200	205	
Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro			
210	215	220	
Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp			
225	230	235	240
Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser			
245	250	255	
Phe Arg Ser Ala Phe Leu Thr Val Leu Pro			
260	265		

&lt;210&gt; 58

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 58

atgacgcccga	gccccctgtt	gctgctcctg	ctgcccgcgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgcccagg	ccccccaaag	atggcggaca	aggtggtccc	acggcagggt	120
gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgttgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggg	aggagagcct	ggggcccgac	agtcctctg	ggggtaaga	ggaccccgcc	420
agccagcagt	ggg					433

&lt;210&gt; 59

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 59

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu					
1	5	10	15		
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala					
20	25	30			
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg					
35	40	45			
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr					
50	55	60			
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu					
65	70	75	80		
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val					
85	90	95			
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr					
100	105	110			

## CONFIDENTIAL

Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly  
 115 120 125  
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp  
 130 135 140

<210> 60

<211> 637

<212> DNA

<213> Human

<400> 60

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ccccggctgg	gccgcactgt	gcccgtgcag	tgcccagtgg	agggggaccc	gccggccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcgct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcg	aactacaccc	tcgtcgtgct	ggcacgaccg	360
cgcttcacac	agccctccaa	gatgaggcgc	cgggtgatcg	cacggcccgt	ggtagctcc	420
gtgcggctca	agtgcgtggc	cagcgggcac	cctcgccccg	acatcacgtg	gatgaaggac	480
gaccaggcct	tgacgcgccc	agaggccgct	gagcccagga	agaagaagtg	gacactgagc	540
ctgaagaacc	tgcggccgga	ggacagcggc	aaatacacct	gccgcgtg	gaaccgcg	600
ggcgccatca	acgcccaccta	caaggtggat	gtgatcc			637

<210> 61

<211> 212

<212> PRT

<213> Human

<400> 61

Met	Thr	Pro	Ser	Pro	Leu							
1				5			10			15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro
				20			25			30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg
						35				40		45
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr
						50				55		60
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe
						65				70		75
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp
						85				90		95
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser
						100				105		110
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro
						115				120		125
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val
						130				135		140
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp
						145				150		155
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg
						165				170		175
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser
						180				185		190
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala
						195				200		205
Val	Asp	Val	Ile									
						210						

<210> 62

<211> 706

<212> DNA

<213> Human

## CONFIDENTIAL

&lt;400&gt; 62

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgttga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccacccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggagcggacc	360
cgttccaagc	ccgtgctcac	aggcacgcac	cccgtgaaca	cgacggtgg	cttcgggggg	420
accacgtcct	tccagtgcaa	ggtgcgcagc	gacgtgaagc	cggtgatcca	gtggctgaag	480
cgcgtggagt	acggcggcga	gggcccacac	aactccacca	tcgatgtggg	cggccagaag	540
tttgtggtgc	tgcccacggg	tgacgtgtgg	tcgcggcccg	acggctccta	cctcaataag	600
ctgctcatca	cccggtcccc	ccaggacgt	gcgggcatgt	acatctgcct	tggcgccaac	660
accatgggct	acagcttccg	cagcgccttc	ctcaccgtgc	tgccag		706

&lt;210&gt; 63

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 63

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
1				5				10					15			
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala	
					20				25				30			
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	
						35			40			45				
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	
						50			55			60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	
						65			70			75			80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val	
						85			90			95				
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	
						100			105			110				
Thr	Leu	Val	Val	Leu	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	
						115			120			125				
Thr	His	Pro	Val	Asn	Thr	Thr	val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	
						130			135			140				
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	
						145			150			155			160	
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	
						165			170			175				
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	
						180			185			190				
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	
						195			200			205				
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	
						210			215			220				
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro						
						225			230			235				

&lt;210&gt; 64

&lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 64

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tcctctgggg	gtcaagagga	ccccgcacgc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgaggcgccg	ggtgatcgca	cggcccggtgg	gtagctccgt	gcggctcaag	240
tgcgtggcca	gcgggcaccc	tcggccgcac	atcacgtgg	tgaaggacga	ccaggccttg	300
acgcgcccag	aggccgctga	gcccaggaag	aagaagtgg	cactgagcct	gaagaacctg	360

## CONFIDENTIAL

cggccggagg acagcggcaa atacacctgc cgcgtgtcga accgcgcggg cgccatcaac 420  
 gccacctaca aggtggatgt gatcc 445

<210> 65  
 <211> 148  
 <212> PRT  
 <213> Human

<400> 65  
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly  
 20 25 30  
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro  
 35 40 45  
 Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met  
 50 55 60  
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys  
 65 70 75 80  
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp  
 85 90 95  
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys  
 100 105 110  
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr  
 115 120 125  
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys  
 130 135 140  
 Val Asp Val Ile  
 145

<210> 66  
 <211> 514  
 <212> DNA  
 <213> Human

<400> 66  
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 gtgctcacag gcacgcaccc cgtgaacacg acgggtggact tcggggggac cacgtccttc 180  
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 cgtgcccggcc aggacgatgc gggcatgtac atctgccttg gcgccaaacac catgggctac 420  
 agcttccgca ggcgccttcct caccgtgctg ccag 480  
 514

<210> 67  
 <211> 171  
 <212> PRT  
 <213> Human

<400> 67  
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly  
 20 25 30  
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro  
 35 40 45  
 Ala Ser Gln Gln Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly  
 50 55 60  
 Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe  
 65 70 75 80  
 Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys

## CONFIDENTIAL

Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
100								105					95		
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
115							120					110	125		
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
130						135					140				
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
145						150					155			160	
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
						165				170					

&lt;210&gt; 68

&lt;211&gt; 718

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 68

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gtgatcgac	ggcccgtggg	tagctccgtg	cggctcaagt	gcgtggccag	cgggcaccct	180
cggcccgaca	tcacgtggat	gaaggacgac	caggccttga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagttggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacctacaa	ggtggatgtg	360
atccagcgg	cccgttccaa	gcccgtgctc	acaggcacgc	accccgtgaa	cacgacgggt	420
gacttcgggg	ggaccacgtc	cttccagtgc	aaggtgcgca	gcgacgtgaa	gccggtgatc	480
cagtggctga	agcgcgtgga	gtacggcgcc	gagggccgccc	acaactccac	catcgatgtg	540
ggcggccaga	agtttgggt	gctgcccacg	ggtgacgtgt	ggtcgccggcc	cgacggctcc	600
tacctaata	agctgctcat	caccctgtgcc	cgccaggacg	atgcgggcat	gtacatctgc	660
tttggcgcca	acaccatggg	ctacagcttc	cgcagcgcct	tcctcaccgt	gctgccag	718

&lt;210&gt; 69

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 69

Met	Thr	Pro	Ser	Pro	Leu									
1				5			10			15				
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe
							20		25		30			Thr
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly
							35		40		45			Ser
Ser	val	Arg	Leu	Lys	Cys	val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp
						50		55		60				Ile
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Glu
						65		70		75		80		
Pro	Arg	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu
						85		90			95			
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala
						100		105			110			Ile
Asn	Ala	Thr	Tyr	Lys	Val	Asp	val	Ile	Gln	Arg	Thr	Arg	Ser	Lys
						115		120			125			Pro
val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly
						130		135			140			
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val
						145		150			155			Ile
Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn
						165		170			175			Ser
Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly
						180		185			190			Asp
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile
						195		200			205			Thr

## CONFIDENTIAL

Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn  
 210 215 220  
 Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro  
 225 230 235

&lt;210&gt; 70

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 70

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 gcccggctgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgcccgtg 180  
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240  
 ccgcaggggc tgaaggatgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300  
 gccaccaacg gcttcggcag ccttagcgta aactacaccc tcgtcgtgct gg 352

&lt;210&gt; 71

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 71

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala  
 20 25 30  
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg  
 35 40 45  
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr  
 50 55 60  
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu  
 65 70 75 80  
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val  
 85 90 95  
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr  
 100 105 110  
 Thr Leu Val Val Leu  
 115

&lt;210&gt; 72

&lt;211&gt; 160

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 72

atgacgcccga gccccctgtt gctgctcctg ctgcccgc tgctgctggg ggccttccca 60  
 ccggccgcccgg ccgccccagg tgacatttagc ccagggaaagg agagcctggg gcccgcacagc 120  
 tcctctgggg gtcagagagga ccccgccagc cagcagtggg 160

&lt;210&gt; 73

&lt;211&gt; 53

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 73

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly  
 20 25 30  
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro  
 35 40 45

## CONFIDENTIAL

Ala Ser Gln Gln Trp  
50

<210> 74  
<211> 364  
<212> DNA  
<213> Human

<400> 74  
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ccggccgccc ccgccccgagc acgaccgcgc ttcacacagc cctccaagat gaggcgccgg 120  
gtgatgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180  
cggcccgaca tcacgtggat gaaggacgac caggcctga cgcccccaga ggccgctgag 240  
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300  
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360  
atcc 364

<210> 75  
<211> 121  
<212> PRT  
<213> Human

<400> 75  
Met Thr Pro Ser Pro Leu Leu Leu Leu Pro Pro Leu Leu  
1 5 10 15  
Gly Ala Phe Pro Pro Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr  
20 25 30  
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser  
35 40 45  
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile  
50 55 60  
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu  
65 70 75 80  
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu  
85 90 95  
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile  
100 105 110  
Asn Ala Thr Tyr Lys Val Asp Val Ile  
115 120

<210> 76  
<211> 433  
<212> DNA  
<213> Human

<400> 76  
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gtgaacacga cggtgactt cggggggacc acgtccttcc agtgcaaggt gcgcagcgac 180  
gtgaagccgg tggatccagtg gctgaagcgc gtggagtacg gcgccgaggg cggccacaac 240  
tccaccatcg atgtggcgg ccagaagttt gtgggtctgc ccacgggtga cgtgtggcgc 300  
cggcccgacg gctcctaccc caataagctg ctcatcaccc gtgcccggca ggacgatgcg 360  
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accgtgctgc cag 433

<210> 77  
<211> 144  
<212> PRT  
<213> Human

<400> 77  
Met Thr Pro Ser Pro Leu Leu Leu Leu Pro Pro Leu Leu  
1 5 10 15

## CONFIDENTIAL

Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Glu Arg Thr Arg Ser Lys  
 20 25 30  
 Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly  
 35 40 45  
 Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val  
 50 55 60  
 Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn  
 65 70 75 80  
 Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly  
 85 90 95  
 Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile  
 100 105 110  
 Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala  
 115 120 125  
 Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro  
 130 135 140

&lt;210&gt; 78

&lt;211&gt; 79

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 78

atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca  
 ccggccgccc cccgccccag

60

79

&lt;210&gt; 79

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 79

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu  
 1 5 10 15  
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg  
 20 25

&lt;210&gt; 80

&lt;211&gt; 1590

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 80

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 gcgcgaggac ccccaagaat ggcagacaaa gtggtcccac ggcaggtggc ccgcctggc 120  
 cgcactgtgc ggctacagtg cccagtgag ggggacccac caccgttgc acatgtggacc 180  
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggcttg 240  
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300  
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccagggaaag 360  
 gagagccctg ggccagggtgg ttcttcgggg ggccaggagg acccagccag ccagcagtgg 420  
 gcacggcctc gttcacaca gcccctcaag atgaggcgcc gagtgattgc acggctgtg 480  
 ggtagctctg tgccgctcaa gtgtgtggcc agtgggcacc cacggccaga catcatgtgg 540  
 atgaaggatg accagacctt gacgcacatca gaggcttagt g aacacagaaa gaagaagtgg 600  
 acactgagct tgaagaacctt gaagcctgaa gacagtggca agtacacgtg ccgtgtatct 660  
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 aaggcctgtgc tcacaggac acaccctgtg aacacaacgg tggacttcgg tggacaacg 780  
 tccttccagt gcaagggtgcg cagtgcacgtg aagcctgtga tccagtggtc gaagcgggtg 840  
 gagtacggct ccgaggacg ccacaactcc accattgtg tgggtggcca gaagtttgtg 900  
 gtgttgcaca cgggtgatgt gtggtcacgg cctgatggct cctaccaa caagctgctc 960  
 atctctcggg cccgccagga tgatgctggc atgtacatct gcctaggtgc aaataccatg 1020  
 ggctacagtt tccgtagcgc cttcctcact gtattaccag accccaaacc tccagggcct 1080  
 cctatggctt cttcatcgac atccacaagc ctgccatggc ctgtgggtat cggcatcccc 1140  
 gctgggtgtg tcttcatcct aggactgtg ctgctctggc tttgcccagac caagaagaag 1200

## CONFIDENTIAL

ccatgtgcc	cagcatctac	acttcctgt	cctggcatc	gtccccagg	gacatcccga	1260
gaacgcagt	gtgacaagga	cctgccctca	ttggctgtgg	gcatatgtga	ggagcatgga	1320
tccgcccatt	ccccccagca	catcctggcc	tctggctcaa	ctgctggccc	caagctgtac	1380
cccaagctat	acacagatgt	gcacacacac	acacatacac	acacctgcac	tcacacgctc	1440
tcatgtggag	ggcaaggttc	atcaacacca	gcatgtccac	tatcagtgct	aaatacagcg	1500
aatctccaag	cactgtgtcc	tgaggttaggc	atttgggggc	caaggcaaca	ggttgggaga	1560
attgagaaca	atggaggaag	agtatcttag				1590

<210> 81  
<211> 529  
<212> PRT  
<213> Mouse

<400> 81

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10				15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
					20			25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
					35			40				45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
					50			55			60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					65			70			75			80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85			90				95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
					100			105				110			
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
					115			120			125				
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
					130			135			140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
					145			150			155			160	
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
					165			170				175			
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
					180			185				190			
Ser	Glu	His	Arg	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	
					195			200			205				
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
					210			215			220				
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser
					225			230			235			240	
Lys	Pro	val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe
					245			250				255			
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro
					260			265			270				
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His
					275			280			285				
Asn	Ser	Thr	Ile	Asp	val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr
					290			295			300				
Gly	Asp	Asp	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu
					305			310			315			320	
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly
					325			330				335			
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu
					340			345				350			
Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	
					355			360				365			
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
					370			375			380				
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys

## CONFIDENTIAL

385	390	395	400
Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro			
405	410	415	
Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala			
420	425	430	
Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile			
435	440	445	
Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr			
450	455	460	
Thr Asp Val His Thr His Thr His Thr His Thr Cys Thr His Thr Leu			
465	470	475	480
Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val			
485	490	495	
Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp			
500	505	510	
Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val			
515	520	525	
Ser			

<210> 82  
<211> 1236  
<212> DNA  
<213> Mouse

&lt;400&gt; 82

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccg	tcggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcagggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaaag	360
gagagccctg	ggccagggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcacatca	gaggctagtg	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgcccataa	cgccacctac	aaagtggatg	taatccaccc	caaaccctcca	720
gggcctccta	tggcttcttc	atcgtcatcc	acaaggctgc	catggcctgt	ggtgatcggc	780
atcccagctg	gtgctgtctt	catccttaggc	actgtgctgc	tctggctttg	ccagaccaag	840
aagaagccat	gtgcccacgc	atctacactt	cctgtgcctg	ggcatcgtcc	cccagggaca	900
tcccggaaac	gcagtggtga	caaggacctg	ccctcattgg	ctgtgggcat	atgtgaggag	960
catggatccg	ccatggccccc	ccagcacatc	ctggcctctg	gctcaactgc	tggccccaag	1020
ctgtacccca	agctatacac	agatgtgcac	acacacacac	atacacacac	ctgcactcac	1080
acgctctcat	gtggaggggca	aggttcatca	acaccagcat	gtccactatc	agtgttaaat	1140
acagcgaatc	tccaaggact	gtgtccctgag	gtaggcattt	gggggccaag	gcaacagggtt	1200
gggagaattg	agaacaatgg	aggaagagta	tcttag			1236

<210> 83  
<211> 411  
<212> PRT  
<213> Mouse

&lt;400&gt; 83

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro					
1	5	10	15		
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val					
20	25	30			
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro					
35	40	45			
Val Glu Gly Asp Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg					
50	55	60			
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu					

## CONFIDENTIAL

65	70	75	80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys			
85	90	95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile			
100	105	110	
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser			
115	120	125	
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg			
130	135	140	
Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val			
145	150	155	160
Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro			
165	170	175	
Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala			
180	185	190	
Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys			
195	200	205	
Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly			
210	215	220	
Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile His Pro Lys Pro Pro			
225	230	235	240
Gly Pro Pro Met Ala Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro			
245	250	255	
Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val			
260	265	270	
Leu Leu Trp Leu Cys Gln Thr Lys Lys Pro Cys Ala Pro Ala Ser			
275	280	285	
Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg			
290	295	300	
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu			
305	310	315	320
His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr			
325	330	335	
Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His			
340	345	350	
Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly			
355	360	365	
Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu			
370	375	380	
Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val			
385	390	395	400
Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser			
405	410		

<210> 84  
<211> 1305  
<212> DNA  
<213> Mouse

<400> 84

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gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggcccac	ggcagggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctcg	240
aaggtgaagg	agggtggaggc	cgaggatgcc	ggtgtttatg	tgtcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggaaag	360
gagagccctg	ggccagggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gagcggactc	gttccaagcc	tgtgctcaca	gggacacacc	ctgtgaacac	aacggtggac	480
ttcgggtggga	caacgtcctt	ccagtgcaag	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
tggctgaagc	gggtggagta	cggctccgag	ggacgccaca	actccaccat	tgatgtgggt	600
ggccagaagt	ttgtgggttt	gcccacgggt	gatgtgtggt	cacggcctga	tggctcctac	660
ctcaacaagc	tgctcatctc	tcgggccccgc	cagatgtatg	ctggcatgta	catctgccta	720
ggtcaaata	ccatgggcta	cagttccgt	agcgccctcc	tcactgtatt	accagacccc	780

## CONFIDENTIAL

aaacctccag	ggcctcctat	ggcttctca	tcgtcatcca	caaggctgcc	atggcctgtg	840
gtgatcgca	tcccagctgg	tgctgtcttc	atcctaggca	ctgtgctgct	ctggctttgc	900
cagaccaaga	agaagccatg	tgccccagca	tctacacttc	ctgtgcctgg	gcatcgtccc	960
ccagggacat	cccgagaacg	cagtggtgac	aaggacctgc	cctcattggc	tgtgggcata	1020
tgtgaggagc	atggatccgc	catggccccc	cagcacatcc	tggcctctgg	ctcaactgct	1080
ggccccaagc	tgtacccaa	gctatacaca	gatgtgcaca	cacacacaca	tacacacacc	1140
tgcactcaca	cgctctcatg	tggagggcaa	ggttcatcaa	caccagcatg	tccactatca	1200
gtgctaaata	cagcgaatct	ccaagcactg	tgtcctgagg	taggcatttg	ggggccaagg	1260
caacaggttg	ggagaattga	gaacaatgga	ggaagagtat	cttag		1305

&lt;210&gt; 85

&lt;211&gt; 434

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 85

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
					20				25			30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
					35				40			45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
					50				55			60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					65				70			75			80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85				90			95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
					100				105			110			
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
					115				120			125			
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Glu	Arg	Thr	Arg
					130				135			140			
Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp
					145				150			155			160
Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys
					165				170			175			
Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg
					180				185			190			
His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro
					195				200			205			
Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu
					210				215			220			
Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu
					225				230			235			240
Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val
					245				250			255			
Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser
					260				265			270			
Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala
					275				280			285			
Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys
					290				295			300			
Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro
					305				310			315			320
Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu
					325				330			335			
Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His
					340				345			350			
Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu
					355				360			365			
Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Cys	Thr	His	Thr	

## CONFIDENTIAL

370	375	380
Leu Ser Cys Gly Gly Gln	Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser	
385	390	395
Val Leu Asn Thr Ala Asn Leu Gln Ala	Leu Cys Pro Glu Val Gly Ile	400
405	410	415
Trp Gly Pro Arg Gln Gln Val Gly Arg	Ile Glu Asn Asn Gly Gly Arg	
420	425	430
Val Ser		

&lt;210&gt; 86

&lt;211&gt; 1509

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 86

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccg	tc ggctgaggcg	60
gcgcgaggac	ccccaagaat	ggcagacaaa	gtggtcccac	ggcagg	ttgcgc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggacccac	caccgtt	gac catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgt	ccagggtctg	240
aaggtgaagg	agggtggaggc	cgaggatgcc	ggtgttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagacctt	480
acgcatctag	aggctagtga	acacagaaag	aagaagtgg	cactgagctt	gaagaacct	540
aaggctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	660
caccctgtga	acacaacggt	ggacttcggt	gggacaacgt	ccttccagtg	caagggtgc	720
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgagggacgc	780
cacaactcca	ccattgatgt	gggtggccag	aagtttgtgg	tctctcggc	ccgcccaggat	840
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tgtgcccac	gggtgatgt	900
gatgctggca	tgtacatctg	cctaggtgca	aataccatgg	gctacagttt	ccgtagcgc	960
ttcctcactg	tattaccaga	ccccaaacct	ccagggc	ctatggcttc	ttcatcgtca	1020
tccacaagcc	tgccatggcc	tgtggtgatc	ggcatcccag	ctgggtctgt	tttcatccta	1080
ggcactgtgc	tgctctggct	ttgccagacc	aagaagaagc	catgtgcccc	agcatctaca	1140
cttcctgtgc	ctgggcatcg	tcccccaggg	acatcccag	aacgcagtgg	tgacaaggac	1200
ctgccctcat	tggctgtgg	catatgtgag	gagcatggat	ccgcccattgc	ccccagcac	1260
atcctggcct	ctggctcaac	tgctggcccc	aagctgtacc	ccaagctata	cacagatgt	1320
cacacacaca	cacatacaca	cacctgcact	cacacgtct	catgtggagg	gcaaggttca	1380
tcaacaccag	catgtccact	atcagtgcta	aatacagcga	atctccaagc	actgtgtcct	1440
gaggtaggca	tttgggggccc	aaggcaacag	gttggagaa	ttgagaacaa	tggaggaaga	1500
gtatcttag						1509

&lt;210&gt; 87

&lt;211&gt; 502

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 87

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1															15
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
															20
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
															35
Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
															50
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
															65
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
															85
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
															100
															105
															110

## CONFIDENTIAL

Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val  
 115 120 125  
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser  
 130 135 140  
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu  
 145 150 155 160  
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser  
 165 170 175  
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val  
 180 185 190  
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile  
 195 200 205  
 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn  
 210 215 220  
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg  
 225 230 235 240  
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly  
 245 250 255  
 Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe  
 260 265 270  
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr  
 275 280 285  
 Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met  
 290 295 300  
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala  
 305 310 315 320  
 Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala  
 325 330 335  
 Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile  
 340 345 350  
 Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys  
 355 360 365  
 Gln Thr Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro  
 370 375 380  
 Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp  
 385 390 395 400  
 Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met  
 405 410 415  
 Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu  
 420 425 430  
 Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr  
 435 440 445  
 Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala  
 450 455 460  
 Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro  
 465 470 475 480  
 Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn  
 485 490 495  
 Asn Gly Gly Arg Val Ser  
 500

&lt;210&gt; 88

&lt;211&gt; 1317

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 88

atgacgcccga gccccgcgct gctgctgctg ctattggggg ccctcccgct ggctgaggcg  
 60  
 gcgcgagatg atattagtcc agggaaaggag agccctgggc caggtggttc ttcggggggc  
 120  
 caggaggacc cagccagcca gcagtggca cggcctcgct tcacacagcc ctccaaagatg  
 180  
 aggccggccag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt  
 240  
 gggcaccacat ggccagacat catgtggatg aaggatgacc agaccttgac gcatcttagag  
 300  
 gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacacctgaa gcctgaagac  
 360

## CONFIDENTIAL

agtggcaagt	acacgtgccg	tgtatctaac	aaggccggtg	ccatcaacgc	cacccataaa	420
gtggatgtaa	tccagccggac	tcgttccaag	cctgtgctca	cagggacaca	ccctgtgaac	480
acaacgggtgg	acttcgggtgg	gacaacgtcc	ttccagtgca	aggtgcgcag	tgacgtgaag	540
cctgtgatcc	agtggctgaa	gcgggtggag	tacggctcg	agggacgcca	caactccacc	600
attgtatgtgg	gtggccagaa	gtttgtggtg	ttgcccacgg	gtgatgtgtg	gtcacggcct	660
gatggctcct	acctcaacaa	gctgctcatc	tctcgggccc	gccaggatga	tgctggcatg	720
tacatctgcc	taggtgcaaa	taccatgggc	tacagttcc	gtagcgcctt	cctcaactgta	780
ttaccagacc	ccaaacctcc	agggcctcct	atggcttctt	catcgcatc	cacaaggcctg	840
ccatggcctg	tggtgatcg	catcccagct	ggtgctgtct	tcatcctagg	cactgtgctg	900
ctctggcttt	gccagaccaa	gaagaagcca	tgtgccccag	catctacact	tcctgtgcct	960
gggcatcg	cccccaggac	atcccagaa	cgcagtgg	acaaggacct	gccctcattg	1020
gctgtgggca	tatgtgagga	gcatggatcc	gccatggccc	cccagcacat	cctggcctct	1080
ggctcaactg	ctggcccaa	gctgtacccc	aagctataca	cagatgtgca	cacacacaca	1140
catacacaca	cctgcactca	cacgctctca	tgtggagggc	aagttcatc	aacaccagca	1200
tgtccactat	cagtgctaaa	tacagcgaat	ctccaaggcac	tgtgtcctga	ggttaggcatt	1260
tggggccaa	ggcaacaggt	tgggagaatt	gagaacaatg	gaggaagagt	atcttag	1317

&lt;210&gt; 89

&lt;211&gt; 438

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 89

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
								20		25			30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
								35		40			45		
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
								50		55			60		
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
								65		70			75		80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
								85		90			95		
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
								100		105			110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
								115		120			125		
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
								130		135			140		
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
								145		150			155		160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
								165		170			175		
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
								180		185			190		
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
								195		200			205		
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
								210		215			220		
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
								225		230			235		240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
								245		250			255		
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala
								260		265			270		
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
								275		280			285		
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys
								290		295			300		
Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro
								305		310			315		320

## CONFIDENTIAL

Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp  
 325 330 335  
 Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met  
 340 345 350  
 Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu  
 355 360 365  
 Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr  
 370 375 380  
 Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala  
 385 390 395 400  
 Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro  
 405 410 415  
 Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn  
 420 425 430  
 Asn Gly Gly Arg Val Ser  
 435

&lt;210&gt; 90

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 90

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccg	tcggctggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcagggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaaag	360
gagagccctg	ggccagggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gaccccaaac	ctccaggggcc	tcctatggct	tcttcatcgt	catccacaag	cctggcatgg	480
cctgtggtga	tcggcatccc	agctggtgct	gtcttcatcc	taggcactgt	gctgctctgg	540
cttgccaga	ccaagaagaa	gccatgtgcc	ccagcatcta	cacttcctgt	gcctgggcat	600
cgtccccca	ggacatcccg	agaacgcagt	ggtgacaagg	acctgccctc	attggctgtg	660
ggcatatgtg	aggagcatgg	atccgccccatg	gccccccagc	acatcctggc	ctctggctca	720
actgctggcc	ccaagctgta	cccccaagcta	tacacagatg	tgcacacaca	cacacataca	780
cacacctgca	ctcacacgct	ctcatgtgga	gggcaaggtt	catcaacacc	agcatgtcca	840
ctatcagtgc	taaatacagc	aatctccaa	gcactgtgtc	ctgaggtagg	catttggggg	900
ccaaggcaac	agggtggag	aattgagaac	aatggaggaa	gagtatctta	g	951

&lt;210&gt; 91

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 91

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10				15		
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
					20				25				30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
					35				40				45		
Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
					50				55				60		
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					65				70				75		80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85				90				95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
					100				105				110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
					115				120				125		
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Asp	Pro	Lys	Pro

## CONFIDENTIAL

130	135	140													
Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp
145				150						155				160	
Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr
165										170				175	
Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala
180								185						190	
Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu
195								200						205	
Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu
210								215						220	
Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser
225								230						240	
Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr
245								250						255	
His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln
260								265						270	
Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn
275								280						285	
Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln
290								295						300	
Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser				
305								310						315	

&lt;210&gt; 92

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 92

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gcgcgaggac	ccccagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgc	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	ttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcatctag	aggctagtga	acacagaaag	aagaagtgg	cactgagctt	gaagaacctg	540
aaggcctgaag	acagtggcaa	gtacacgtgc	cgtgttatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccacccc	aaacctccag	ggcctcctat	ggcttcttca	660
tcgtcatcca	caagcctgcc	atggcctgtg	gtgatcg	tcccagctgg	tgctgtcttc	720
atcctaggca	ctgtgctgct	ctggccttgc	cagaccaaga	agaagccatg	tgccccagca	780
tctacacttc	ctgtgcctgg	gcatcg	ccagggacat	cccgagaacg	cagtgggtac	840
aaggacctgc	cctcattggc	tgtgggcata	tgtgaggagc	atggatccgc	catggcccc	900
cagcacatcc	tggcctctgg	ctcaactgct	ggcccaagc	tgtacccaa	gctatacaca	960
gatgtgcaca	cacacacaca	tacacacacc	tgcactcaca	cgctctcatg	tggagggcaa	1020
ggttcatcaa	caccagcatg	tccactatca	gtgctaaata	cagcgaatct	ccaagcactg	1080
tgtcctgagg	taggcatttg	ggggccaagg	caacaggttg	ggagaattga	gaacaatgga	1140
ggaagagtat	cttag					1155

&lt;210&gt; 93

&lt;211&gt; 384

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 93

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1														15
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
20								25					30	
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
35								40					45	

## CONFIDENTIAL

Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg  
 50 55 60  
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu  
 65 70 75 80  
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys  
 85 90 95  
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile  
 100 105 110  
 Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val  
 115 120 125  
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser  
 130 135 140  
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu  
 145 150 155 160  
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser  
 165 170 175  
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val  
 180 185 190  
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile  
 195 200 205  
 His Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Thr  
 210 215 220  
 Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe  
 225 230 235 240  
 Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro  
 245 250 255  
 Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly  
 260 265 270  
 Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val  
 275 280 285  
 Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu  
 290 295 300  
 Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr  
 305 310 315 320  
 Asp Val His Thr His Thr His Thr His Thr Cys Thr His Thr Leu Ser  
 325 330 335  
 Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu  
 340 345 350  
 Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly  
 355 360 365  
 Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser  
 370 375 380

<210> 94  
 <211> 1224  
 <212> DNA  
 <213> Mouse

<400> 94

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cgcactgtgc	ggctacagtg	cccagtgag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctcg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	agcggactcg	ttccaagcct	360
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cagtgcaagg	tgcgcagtga	cgtgaagcct	gtgatccagt	ggctgaagcg	ggtggagttac	480
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cccacgggtg	atgtgtggtc	acggcctgat	ggctcctacc	tcaacaagct	gctcatctct	600
cgggcccccc	aggatgatgc	tggcatgtac	atctgcctag	gtgcaaatac	catgggctac	660
agtttccgta	gcgccttcct	cactgtattt	ccagacccca	aacctccagg	gcctcctatg	720
gcttcttcat	cgtcatccac	aagcctgcca	tggcctgtgg	tgatcggcat	cccagctggt	780
gctgtttca	tccttaggcac	tgtgctgctc	tggcttgcc	agaccaagaa	gaagccatgt	840

## CONFIDENTIAL

gccccagcat	ctacacttcc	tgtgcctggg	catcgcccc	cagggacatc	ccgagaacgc	900
agtggtgaca	aggacctgcc	ctcattggct	gtggccatat	gtgaggagca	tggatccgccc	960
atggccccc	agcacatcct	ggcctctggc	tcaactgctg	gccccaaagct	gtaccccaag	1020
ctatacacag	atgtgcacac	acacacacat	acacacacat	gcactcacac	gctctcatgt	1080
ggagggcaag	gttcatcaac	accagcatgt	ccactatcag	tgctaaatac	agcgaatctc	1140
caagcactgt	gtcctgaggt	aggcatttg	ggccaaggc	aacaggttgg	gagaatttag	1200
aacaatggag	gaagagtac	ttag				1224

&lt;210&gt; 95

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 95

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10				15		
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
							20		25				30	
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
							35		40			45		
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
							50		55			60		
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
							65		70			75		80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
							85		90			95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
							100		105			110		
Met	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro
							115		120			125		Val
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys
							130		135			140		
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
							145		150			155		Tyr
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln
							165		170			175		Lys
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly
							180		185			190		Ser
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala
							195		200			205		Gly
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Gly	Tyr	Ser	Phe	Arg	Ser
							210		215			220		
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro
							225		230			235		Met
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile
							245		250			255		Gly
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp
							260		265			270		Leu
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro
							275		280			285		Val
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp
							290		295			300		Lys
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser
							305		310			315		Ala
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro
							325		330			335		Lys
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr
							340		345			350		His
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr
							355		360			365		Pro
Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu
							370		375			380		Cys
Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile

CONFIDENTIAL

385 Asn Asn Gly Gly Arg Val Ser  
390  
405

400

<210> 96  
<211> 963  
<212> DNA  
<213> M011

<400> 96

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caggaggacc	cagccagcca	gcagtggca	cggcctcgct	tcacacagcc	ctccaagatg	180
aggcgccgag	tgattgcacg	gcctgtgggt	agctctgtgc	ggctcaagtg	tgtggccagt	240
gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
agtggcaagt	acacgtgccg	tgtatctaac	aaggccggtg	ccatcaacgc	cacctacaaa	420
gtggatgtaa	tccaccccaa	acctccaggg	cctcctatgg	cttcttcatc	gtcatccaca	480
agcctgccat	ggcctgtggt	gatcggcatc	ccagctggtg	ctgtcttcat	cctaggcact	540
gtgctgctct	ggcttgcca	gaccaagaag	aagccatgtg	ccccagcatc	tacacttcct	600
gtgcctggc	atcgcccccc	agggacatcc	cgagaacgca	gtggtgacaa	ggacctgccc	660
tcattggctg	tgggcatatg	tgaggagcat	ggatccgcca	tggcccccca	gcacatcctg	720
gcctctggct	caactgctgg	ccccaaagctg	taccccaagc	tatacacaga	tgtgcacaca	780
cacacacata	cacacacac	cactcacacg	ctctcatgtg	gagggcaagg	ttcatcaaca	840
ccagcatgtc	caactatcgt	gctaaataca	gcgaatctcc	aagcactgtg	tcctgaggt	900
ggcattttggg	ggccaaggca	acaggttggg	agaattgaga	acaatggagg	aagagtatct	960
tag						963

<210> 97

<211> 320

<212> PRT

<213> Mouse

<400> 97

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5					10				15		
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
				20					25				30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
				35			40					45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
				50		55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
				65		70				75				80	
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85					90				95		
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
				100				105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
				115			120					125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
				130		135					140				
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr
				145		150				155				160	
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe
				165					170				175		
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro
				180				185				190			
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly
				195				200				205			
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val
				210		215					220				
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu

## CONFIDENTIAL

225	230	235	240
Ala Ser Gly Ser Thr Ala Gly Pro Lys	Leu Tyr Pro Lys Leu Tyr Thr		
245	250	255	
Asp Val His Thr His Thr His Thr	Cys Thr His Thr Leu Ser		
260	265	270	
Cys Gly Gly Gln Gly Ser Ser Thr	Pro Ala Cys Pro Leu Ser val Leu		
275	280	285	
Asn Thr Ala Asn Leu Gln Ala	Leu Cys Pro Glu Val Gly Ile Trp Gly		
290	295	300	
Pro Arg Gln Gln val Gly Arg Ile Glu Asn Asn	Gly Gly Arg Val Ser		
305	310	315	320

<210> 98  
<211> 1032  
<212> DNA  
<213> Mouse

&lt;400&gt; 98

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccg	tcggctggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctggc	caggtgg	ttcgggggc	120
caggaggacc	cagccagcca	gcagtggag	cggactcg	ccaagcctgt	gctcacaggg	180
acacaccctg	tgaacacaac	ggtggacttc	ggtggacaa	cgtccttcca	gtgcaaggtg	240
cgcagtgacg	tgaagcctgt	gatccagtgg	ctgaagcggg	tggagtacgg	ctccgaggga	300
cgcacacaact	ccaccattga	tgtgggtggc	cagaagttt	tggtgttgc	cacgggtat	360
gtgtggtcac	ggcctgatgg	ctccttac	aacaagctgc	tcatctctcg	ggcccgccag	420
gatgatgctg	gcatgtacat	ctgccttagt	gcaaatacca	tgggctacag	tttccgtac	480
gccttcctca	ctgttattacc	agacccaaa	cctccagg	ctccttatggc	ttcttcatcg	540
tcatccacaa	gcctgccatg	gcctgtgg	atcggcatcc	cagctgg	tgtcttcatc	600
ctaggcactg	tgctgctctg	gctttgccag	accaagaaga	agccatgtgc	cccagcatct	660
acacttcctg	tgcctggca	tcgtccccca	gggacatccc	gagaacgcag	tggtgacaag	720
gacctgccc	cattggctgt	gggcataatgt	gaggagcatg	gatccgccc	ggccccccag	780
cacatcctgg	cctctggctc	aactgctggc	cccaagctgt	accccaagct	atacacagat	840
gtgcacacac	acacacatac	acacacactgc	actcacacgc	tctcatgtgg	agggcaaggt	900
tcatcaacac	cagcatgtcc	actatcagt	ctaaatacag	cgaatctcca	agcactgtgt	960
cctgaggtag	gcatttgggg	gccaaggcaa	caggtgg	gaattgagaa	caatggagga	1020
agagtatctt	ag					1032

<210> 99  
<211> 343  
<212> PRT  
<213> Mouse

&lt;400&gt; 99

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu	Gly Ala Leu Pro		
1	5	10	15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro	Gly Lys Glu Ser Pro		
20	25	30	
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro	Ala Ser Gln Gln		
35	40	45	
Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr	Gly Thr His Pro Val		
50	55	60	
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser	Phe Gln Cys Lys Val		
65	70	75	80
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys	Arg Val Glu Tyr		
85	90	95	
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val	Gly Gln Lys		
100	105	110	
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg	Pro Asp Gly Ser		
115	120	125	
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln	Asp Asp Ala Gly		
130	135	140	
Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly	Tyr Ser Phe Arg Ser		
145	150	155	160

## CONFIDENTIAL

Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met  
 165 170 175  
 Ala Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly  
 180 185 190  
 Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu  
 195 200 205  
 Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val  
 210 215 220  
 Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys  
 225 230 235 240  
 Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala  
 245 250 255  
 Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys  
 260 265 270  
 Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His  
 275 280 285  
 Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro  
 290 295 300  
 Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys  
 305 310 315 320  
 Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu  
 325 330 335  
 Asn Asn Gly Gly Arg Val Ser  
 340

&lt;210&gt; 100

&lt;211&gt; 1236

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 100

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagcac	ggcctcgctt	cacacagccc	tccaagatga	ggcgccgagt	gattgcacgg	120
cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagtg	ggcacccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaagaag	240
aagtggacac	tgagcttgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccgggtgc	catcaacgcc	acctacaag	tggatgtaat	ccagcggact	360
cgttccaagc	ctgtgctcac	agggacacac	cctgtgaaca	caacgtgga	cttcgggtggg	420
acaacgtcct	tccagtgcaa	ggtgcgcagt	gacgtgaagc	ctgtgatcca	gtggctgaag	480
cgggtggagt	acggctccga	gggacgccac	aactccacca	ttgatgtggg	tggccagaag	540
tttgtggtgt	tgcccacggg	tgatgtgtgg	tcacggcctg	atggctccta	cctcaacaag	600
ctgctcatct	ctcggggcccg	ccaggatgat	gctggcatgt	acatctgcct	aggtgcaaat	660
accatgggct	acagttccg	taggccttc	ctcactgtat	taccagaccc	caaacctcca	720
gggcctccta	tggcttcttc	atcgcatcc	acaaggctgc	catggcctgt	ggtgatcggc	780
atcccagctg	gtgctgtctt	catccttaggc	actgtgctgc	tctggcttg	ccagaccaag	840
aagaagccat	gtgccccagc	atctacactt	cctgtgcctg	ggcatcggtcc	cccagggaca	900
tcccgagaac	gcagtggtga	caaggacctg	ccctcattgg	ctgtggcat	atgtgaggag	960
catggatccg	ccatggcccc	ccagcacatc	ctggcctctg	gctcaactgc	tggccccaaag	1020
ctgtacccca	agctatacac	agatgtgcac	acacacacac	atacacacac	ctgcactcac	1080
acgctctcat	gtggagggca	agttcatca	acaccagcat	gtccactatc	agtgctaaat	1140
acagcgaatc	tccaagcact	gtgtcctgag	gtaggcattt	gggggccaag	gcaacaggtt	1200
gggagaattg	agaacaatgg	aggaagagta	tcttag			1236

&lt;210&gt; 101

&lt;211&gt; 411

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 101

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1														15	
Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
								20	25			30			

## CONFIDENTIAL

Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu  
 35 40 45  
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys  
 50 55 60  
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys  
 65 70 75 80  
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys  
 85 90 95  
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr  
 100 105 110  
 Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly  
 115 120 125  
 Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe  
 130 135 140  
 Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys  
 145 150 155 160  
 Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val  
 165 170 175  
 Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg  
 180 185 190  
 Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln  
 195 200 205  
 Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr  
 210 215 220  
 Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro  
 225 230 235 240  
 Gly Pro Pro Met Ala Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro  
 245 250 255  
 Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val  
 260 265 270  
 Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser  
 275 280 285  
 Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg  
 290 295 300  
 Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu  
 305 310 315 320  
 His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr  
 325 330 335  
 Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His  
 340 345 350  
 Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly  
 355 360 365  
 Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu  
 370 375 380  
 Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val  
 385 390 395 400  
 Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser  
 405 410

&lt;210&gt; 102

&lt;211&gt; 870

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 102

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	accccaaacc	tccagggcct	360
cctatggctt	cttcatcgtc	atccacaagc	ctgccatggc	ctgtggtgat	cggcatccca	420
gctggtgctg	tcttcatcct	aggcactgtg	ctgctctggc	tttgccagac	caagaagaag	480

## CONFIDENTIAL

ccatgtgccc	cagcatctac	acttcctgtg	cctggcattc	gtccccagg	gacatcccga	540
gaacgcagtg	gtgacaagga	cctgcctca	ttggctgtgg	gcatatgtga	ggagcatgga	600
tccgccatgg	ccccccagca	catcctggcc	tctggctcaa	ctgctggccc	caagctgtac	660
cccaagctat	acacagatgt	gcacacacac	acacatacac	acacctgcac	tcacacgctc	720
tcatgtggag	ggcaaggttc	atcaacacca	gcatgtccac	tatcagtgtct	aaatacagcg	780
aatctccaag	cactgtgtcc	tgaggttaggc	atttgggggc	caaggcaaca	ggttgggaga	840
attgagaaca	atggaggaag	agtatcttag				870

&lt;210&gt; 103

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 103

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
					20				25				30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
					35				40			45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
					50				55			60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					65				70			75			80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85				90			95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
					100				105			110			
Met	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser
					115				120			125			
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
					130				135			140			
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys
					145				150			155			160
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
					165				170			175			
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala
					180				185			190			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile
					195				200			205			
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
					210				215			220			
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu
					225				230			235			240
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val
					245				250			255			
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp
					260				265			270			
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val
					275				280			285			
Ser															

&lt;210&gt; 104

&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 104

atgacgcgga	cccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctgggc	caggtggttc	ttcggggggc	120
caggaggacc	cagccagcca	gcagtggac	cccaaacctc	cagggcctcc	tatggcttct	180
tcatcgatcat	ccacaaggct	gccatggcct	gtggatcg	gcatcccagc	tggtgctgtc	240

## CONFIDENTIAL

ttcatcctag	gcactgtgct	gctctggctt	tgccagacca	agaagaagcc	atgtccccca	300
gcatctacac	ttcctgtgcc	tggcatcg	cccccaggga	catcccgaga	acgcagtgg	360
gacaaggacc	tgccctcatt	ggctgtggc	atatgtgagg	agcatggatc	cgccatggcc	420
ccccagcaca	tcctggcctc	tggctcaact	gctggcccca	agctgtaccc	caagctatac	480
acagatgtc	acacacacac	acatacacac	acctgcactc	acacgctctc	atgtggaggg	540
caaggttcat	caacaccagc	atgtccacta	tcagtgtcaa	atacagcgaa	tctccaagca	600
ctgtgtcctg	aggtaggcat	ttgggggcca	aggcaacagg	ttgggagaat	tgagaacaat	660
ggaggaagag	tatcttag					678

&lt;210&gt; 105

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 105

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
					20				25			30			
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
					35				40			45			
Trp	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser
					50				55			60			
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
					65				70			75			80
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys
					85				90			95			
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
					100				105			110			
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala
					115				120			125			
val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile
					130				135			140			
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
					145				150			155			160
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu
					165				170			175			
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val
					180				185			190			
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp
					195				200			205			
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val
					210				215			220			
Ser															
225															

&lt;210&gt; 106

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 106

atgacgcgga	cccccgcgct	gctgctgctg	ctattgggg	ccctcccg	ggctgaggcg	60
gcgcgagcac	ggcctcgctt	cacacagccc	tccaagatga	ggcgccgagt	attgcacgg	120
cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagtg	ggcacccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaagaag	240
aagtggacac	tgagcttgaa	gaacctgaa	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccggtgc	catcaacgccc	acctacaaag	tggatgtaat	ccaccccaa	360
cctccagggc	ctccttatggc	ttcttcatcg	tcatccacaa	gcctgccatg	gcctgtggtg	420
atcggcatcc	cagctgggtgc	tgtcttcatc	ctaggcactg	tgctgctctg	gcttgc	480
accaagaaga	agccatgtgc	cccagcatct	acacttcctg	tgcctggca	tcgtccccca	540
gggacatccc	gagaacgcag	tggtgacaag	gacctgcct	cattggctgt	gggcataatgt	600
gaggagcatg	gatccgccc	ggccccccag	cacatccctgg	cctctggctc	aactgctggc	660

## CONFIDENTIAL

cccaagctgt	accccaagct	atacacagat	gtgcacacac	acacacatac	acacacctgc	720
actcacacgc	tctcatgtgg	agggcaaggt	tcatcaacac	cagcatgtcc	actatcagtg	780
ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	gcatttgggg	gccaggcaa	840
caggttggga	gaattgagaa	caatggagga	agagtatctt	ag		882

<210> 107  
<211> 293  
<212> PRT  
<213> Mouse

<400> 107

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10				15			
Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
		20					25					30			
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu
	35					40					45				
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys
	50				55					60					
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys
65				70				75				80			
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys
		85				90						95			
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr
	100					105					110				
Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser
	115					120					125				
Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro
	130				135					140					
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln
145				150				155				160			
Thr	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	
		165					170					175			
His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu
	180					185						190			
Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala
	195					200					205				
Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr
210				215					220						
Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys
225				230				235				240			
Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys
		245					250					255			
Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu
	260					265			270			270			
Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn
	275					280					285				
Gly	Gly	Arg	Val	Ser											
	290														

<210> 108  
<211> 951  
<212> DNA  
<213> Mouse

<400> 108

atgacgcgga	ccccgcgct	gctgctgctg	ctattgggg	ccctcccg	ggctgaggcg	60
gcgcgagagc	gactcg	caagcctgtg	ctcacagg	cacacc	gaacacaacg	120
gtggacttcg	gtgggacaac	gtccttccag	tgcaagg	gcagt	gaaggctgt	180
atccagttgc	tgaagcggt	ggagtacggc	tccgagg	gccaactc	caccatt	240
gtgggtggcc	agaagt	ttgttgc	acgggtgat	tgtgg	cacgtatggc	300
tcctacatca	acaagctg	catctctcg	atgatg	tcac	tgtattacca	360
tgcctaggt	caaataccat	ggctacagt	ttccgt	ccttc		420

## CONFIDENTIAL

gacccaaac	ctccagggcc	tcctatggct	tcttcatcg	catccacaag	cctgccatgg	480
cctgtggta	tcggcatccc	agctggtgct	gtttcatcc	taggcactgt	gctgctctgg	540
cttgcaga	ccaagaagaa	gccatgtgcc	ccagcatcta	cacttcctgt	gcctgggcat	600
cgtccccag	ggacatcccg	agaacgcagt	ggtgacaagg	acctgccctc	attggctgtg	660
ggcatatgtg	aggagcatgg	atccgccatg	gccccccagc	acatcctggc	ctctggctca	720
actgctgcc	ccaagctgta	ccccaaagcta	tacacagatg	tgcacacaca	cacacataca	780
cacacctgca	ctcacacgct	ctcatgtgga	gggcaaggtt	catcaacacc	agcatgtcca	840
ctatcgtgc	taaatacagc	aatctccaa	gcactgtgtc	ctgaggtagg	cattttggggg	900
ccaaggcaac	aggttggag	aattgagaac	aatggaggaa	gagtatctta	g	951

&lt;210&gt; 109

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 109

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1															15
Ser	Ala	Glu	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr
								20							30
Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser
															35
Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu
															50
Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp
															65
65	70	75	80												
val	Gly	Gly	Gln	Lys	Phe	val	val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser
															85
Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg
															100
Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
															115
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro
															130
Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	
															145
145	150	155	160												
Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr
															165
165	170	175													
val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala
															180
180	185	190													
Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu
															195
195	200	205													
Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu
															210
210	215	220													
Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser
															225
225	230	235													
Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr
															245
245	250	255													
His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln
															260
260	265	270													
Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn
															275
275	280	285													
Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln
															290
290	295	300													
Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser				
															305
305	310	315													

&lt;210&gt; 110

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 110

**CONFIDENTIAL**

atgacgcgga	gccccgcgt	gctgctgctg	ctattgggg	ccctcccg	ggctgaggcg	60
gcgcgagacc	ccaaacctcc	agggcctcct	atggcttctt	catcgcatc	cacaagcctg	120
ccatggcctg	tggtgatcg	catcccagct	ggtgctgtct	tcatcctagg	cactgtgctg	180
ctctggcttt	gccagaccaa	gaagaagcca	tgtgccccag	catctacact	tcctgtgcct	240
ggcgcattgtc	ccccagggac	atcccggaa	cgcagtgg	acaaggacct	gccctcattg	300
gctgtggca	tatgtgagga	gcatggatcc	gccatggccc	cccagcacat	cctggcctct	360
ggctcaactg	ctggcccaa	gctgtacccc	aagctataca	cagatgtgca	cacacacaca	420
catacacaca	cctgcactca	cacgctctca	tgtggaggc	aaggttcatc	aacaccagca	480
tgtccactat	cagtgctaaa	tacagcgaat	ctccaagcac	tgtgtcctga	ggtaggcatt	540
tggggccaa	ggcaacaggt	tgggagaatt	gagaacaatg	gaggaagagt	atcttag	597

<210> 111

<211> 198

<212> PRT

<213> Mouse

<400> 111

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10					15
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met Ala
								20		25				30
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly Ile
								35		40				45
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu Cys
								50		55				60
Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val Pro
65						70					75			80
Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys Asp
						85				90				95
Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala Met
								100		105				110
Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys Leu
								115		120				125
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His Thr
								130		135				140
Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro Ala
145											155			160
Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys Pro
										165				175
Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu Asn
								180		185				190
Asn	Gly	Gly	Arg	Val	Ser									
								195						

<210> 112

<211> 1060

<212> DNA

<213> Mouse

<400> 112

atgacgcgga	cccccgcgct	gctgctgctg	ctattgggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgcac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcatcta	gaggctagtg	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccagcg	gactcggtcc	720
aagcctgtgc	tcacagggac	acaccctqtg	aacacaacqq	tqqacttcqq	tqqqacaacq	780

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tccttccagt gcaagggtgcg cagtgacgtg aagcctgtga tccagttggct gaagcgggtg	840
gagttacggct ccgagggacg ccacaactcc accattgtatg tgggtggcca gaagtttgg	900
gtgttgcggc cgggtgtatgt gtggcacgg cctgatggct cctaccta caagctgctc	960
atctctcggtt cccgcccaggatgtatgctggc atgtacatct gccttaggtgc aaataccatg	1020
ggctacagtt tccgtacgc cttccctact gtattaccag	1060

&lt;210&gt; 113

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 113

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1 5 10 15	
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20 25 30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100 105 110	
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser	
115 120 125	
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg	
130 135 140	
Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val	
145 150 155 160	
Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro	
165 170 175	
Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala	
180 185 190	
Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys	
195 200 205	
Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly	
210 215 220	
Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser	
225 230 235 240	
Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe	
245 250 255	
Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro	
260 265 270	
Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His	
275 280 285	
Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr	
290 295 300	
Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu	
305 310 315 320	
Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly	
325 330 335	
Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu	
340 345 350	
Pro	

&lt;210&gt; 114

&lt;211&gt; 706

&lt;212&gt; DNA

&lt;213&gt; Mouse

## CONFIDENTIAL

<400> 114

atgacgcgga	ccccgcgct	gctgctgctg	ctattgggg	ccctcccg	ggctgaggcg	60
gcgcgaggac	ccccagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctggc	120
cgcaactgtc	ggctacagt	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaaag	360
gagagccctg	ggccagggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacatt	gacgcaccta	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgcccataa	cggcacctac	aaagtggatg	taatcc		706

<210> 115

<211> 235

<212> PRT

<213> Mouse

<400> 115

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5			10				15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
							20		25				30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
							35		40			45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
							50		55			60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
							65		70			75			80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
							85		90			95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
							100		105			110			
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
							115		120			125			
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
							130		135			140			
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
							145		150			155			160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
							165		170			175			
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
							180		185			190			
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
							195		200			205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
							210		215			220			
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile					
							225		230			235			

<210> 116

<211> 775

<212> DNA

<213> Mouse

<400> 116

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gcgcgaggac	ccccagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctggc	120
cgcaactgtc	ggctacagt	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgttatg	tgtgcaaggc	caccaatggc	300

## CONFIDENTIAL

tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggaaag	360
gagagccctg	ggccagggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gagcggactc	gttccaagcc	tgtgctcaca	gggacacacc	ctgtgaacac	aacgggtggac	480
ttcgggtggaa	caacgtcctt	ccagtgcaga	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
tggctgaagc	gggtggagta	cggctccgag	ggacgcccaca	actccaccat	tgatgtgggt	600
ggccagaagt	ttgtgggttt	gcccacgggt	gatgtgtggt	cacggcctga	tggctcctac	660
ctcaacaagc	tgctcatctc	tcgggcccgc	caggatgatg	ctggcatgta	catctgccta	720
ggtgcaaata	ccatgggcta	cagttccgt	agcgccttcc	tcactgtatt	accag	775

&lt;210&gt; 117

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 117

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
									25				30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
									40			45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
									50			60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
									70			75			80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
									85			90			95
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
									100			105			110
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
									115			120			125
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Glu	Arg	Thr	Arg
									130			135			140
Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp
									145			150			160
Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys
									165			170			175
Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg
									180			185			190
His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro
									195			200			205
Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu
									210			215			220
Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu
									225			230			235
Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val
									245			250			255
Leu	Pro														

&lt;210&gt; 118

&lt;211&gt; 979

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 118

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctcg	240
aaggtaagg	aggtaaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420

## CONFIDENTIAL

tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcacatctag	aggctagtga	acacagaaaag	aagaagtggaa	cactgagctt	gaagaacctg	540
aaggcctgaag	acagtggcaa	gtacacgtgc	cgtgttatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccagcgg	actcggttcca	agcctgtgct	cacagggaca	660
caccctgtga	acacaacggt	ggacttcggt	gggacaacgt	ccttccagtg	caagggtgcgc	720
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgagggacgc	780
cacaactcca	ccattgtatgt	gggtggccag	aagtttgtgg	tgttgcccac	gggtgatgtg	840
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgcccaggat	900
gatgctggca	tgtacatctg	cctaggtgca	aataccatgg	gctacagttt	ccgtagcgcc	960
ttcctcactg	tattaccag					979

&lt;210&gt; 119

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 119

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
					20				25			30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
					35				40			45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
					50				55			60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					65				70			75			80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85				90			95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
					100				105			110			
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
					115				120			125			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
					130				135			140			
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
					145				150			155			160
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
					165				170			175			
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
					180				185			190			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
					195				200			205			
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
					210				215			220			
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
					225				230			235			240
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
					245				250			255			
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
					260				265			270			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
					275				280			285			
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
					290				295			300			
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
					305				310			315			320
Phe	Leu	Thr	Val	Leu	Pro										
					325										

&lt;210&gt; 120

&lt;211&gt; 787

&lt;212&gt; DNA

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<213> Mouse

<210> 121

<211> 262

<212> PRT

<213> Mouse

<400> 121

<210> 122

<210> 122

<212> DNA

<212> DNA  
<213> Mouse

## CONFIDENTIAL

<400> 122  
atgacgcgga gccccgcgt gctgctgctg ctattggggg ccctcccgac ggctgaggcg 60  
gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctggc 120  
cgcactgtgc ggctacagtg cccagtgag ggggacccac caccgttgc acatgtggacc 180  
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctg 240  
aaggtgaagg aggtggaggc cgaggatgcc ggtgttatg tgtgcaaggc caccaatggc 300  
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccaggaaag 360  
gagagccctg ggccaggtgg ttcttcgggg ggccaggagg acccagccag ccagcagtgg 420  
g 421

&lt;210&gt; 123

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Mouse

<400> 123  
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro  
1 5 10 15  
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val  
20 25 30  
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro  
35 40 45  
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg  
50 55 60  
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu  
65 70 75 80  
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys  
85 90 95  
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile  
100 105 110  
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser  
115 120 125  
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp  
130 135 140

&lt;210&gt; 124

&lt;211&gt; 625

&lt;212&gt; DNA

&lt;213&gt; Mouse

<400> 124  
atgacgcgga gccccgcgt gctgctgctg ctattggggg ccctcccgac ggctgaggcg 60  
gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctggc 120  
cgcactgtgc ggctacagtg cccagtgag ggggacccac caccgttgc acatgtggacc 180  
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctg 240  
aaggtgaagg aggtggaggc cgaggatgcc ggtgttatg tgtgcaaggc caccaatggc 300  
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg cacggcctcg cttcacacag 360  
ccctccaaga tgaggcgccg agtgattgca cggccgtgg gtagctctgt gcggctcaag 420  
tgtgtggcca gtgggcaccc acggccagac atcatgtgaa tgaaggatga ccagacctg 480  
acgcatctag aggctagtga acacagaaag aagaagtggc cactgagctt gaagaacctg 540  
aagcctgaag acagtggcaa gtacacgtgc cgtgtatcta acaaggccgg tgccatcaac 600  
gccacctaca aagtggatgt aatcc 625

&lt;210&gt; 125

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Mouse

<400> 125  
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro  
1 5 10 15  
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val

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20	25	30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro		
35	40	45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg		
50	55	60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu		
65	70	75
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys		
85	90	95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile		
100	105	110
Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val		
115	120	125
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser		
130	135	140
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu		
145	150	155
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser		
165	170	175
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val		
180	185	190
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile		
195	200	205

&lt;210&gt; 126

&lt;211&gt; 694

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 126

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccg	ggctgaggcg	60
gcgcgaggac	ccccaaat	ggcagacaaa	gtggccac	ggcagg	ccgcctggc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggacccac	caccgtt	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgttcc	gtgtgt	ccaggg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttag	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	agcggactcg	ttccaa	360
gtgctcacag	ggacacaccc	tgtgaacaca	acggtgact	tcgggtggac	aacgtccttc	420
cagtgcaagg	tgcgcagtga	cgtgaagcct	gtgatccagt	ggctgaagcg	ggtggag	480
ggctccgagg	gacgccacaa	ctccaccatt	gatgtgggtg	gccagaagtt	tgtgtgttg	540
cccacgggtg	atgtgtggtc	acggcctgat	ggctcctacc	tcaacaagct	gctcatctct	600
cgggcccggcc	aggatgatgc	tggcatgtac	atctgcctag	gtgcaaatac	catgggctac	660
agtttccgta	gcgccttcct	cactgtatta	ccag			694

&lt;210&gt; 127

&lt;211&gt; 231

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 127

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro			
1	5	10	15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val			
20	25	30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro			
35	40	45	
Val Glu Gly Asp Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg			
50	55	60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu			
65	70	75	80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys			
85	90	95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile			
100	105	110	

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Met Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val  
 115 120 125  
 Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val  
 130 135 140  
 Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr  
 145 150 155 160  
 Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys  
 165 170 175  
 Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser  
 180 185 190  
 Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly  
 195 200 205  
 Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser  
 210 215 220  
 Ala Phe Leu Thr Val Leu Pro  
 225 230

&lt;210&gt; 128

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 128

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctgggc	caggtggttc	ttcggggggc	120
caggaggacc	cagccagcca	gcagtggca	cggcctcgct	tcacacagcc	ctccaagatg	180
aggcggcgag	tgattgcacg	gcctgtgggt	agctctgtgc	ggctcaagtg	tgtggccagt	240
gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
agtggcaagt	acacgtgccc	tgtatctaac	aaggccggtg	ccatcaacgc	cacctacaaa	420
gtggatgtaa	tcc					433

&lt;210&gt; 129

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 129

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro						
1	5	10	15			
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro						
20	25	30				
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln						
35	40	45				
Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val						
50	55	60				
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser						
65	70	75	80			
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu						
85	90	95				
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser						
100	105	110				
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val						
115	120	125				
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile						
130	135	140				

&lt;210&gt; 130

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 130

## CONFIDENTIAL

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccg	tcggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctgggc	caggtggttc	ttcggggggc	120
caggaggacc	cagccagcca	gcagtggag	cggactcg	ccaaggctgt	gctcacaggg	180
acacaccctg	tgaacacaac	ggtggacttc	ggtggacaa	cgtccttcca	gtgcaagg	240
cgcagtgacg	tgaagcctgt	gatccagtgg	ctgaagcggg	tggagtaggg	ctccgaggga	300
cgcacacaact	ccaccattga	tgtgggtggc	cagaagttt	tgggtttgcc	cacgggtgat	360
gtgtggtcac	gcccgtatgg	ctcctacctc	aacaagctgc	tcatctctcg	ggcccggccag	420
gatgatgctg	gcatgtacat	ctgcctaggt	gcaaatacca	tgggtacag	tttccgtac	480
gccttcctca	ctgtattacc	ag				502

&lt;210&gt; 131

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 131

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5						10			15		
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
								20		25			30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
								35		40			45		
Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
								50		55			60		
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
								65		70			75		80
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr
								85		90			95		
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
								100		105			110		
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
								115		120			125		
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
								130		135			140		
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
								145		150			155		160
Ala	Phe	Leu	Thr	Val	Leu	Pro									
								165							

&lt;210&gt; 132

&lt;211&gt; 706

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 132

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccg	tcggctgaggcg	60
gcgcgagcac	ggcctcgctt	cacacagccc	tccaagatga	ggcgccgagt	gattgcacgg	120
cctgtggta	gctctgtgcg	gctcaagtgt	gtggccagt	ggcacccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaagaag	240
aagtggacac	tgagctgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccgggtgc	catcaacgccc	acctacaaag	tggatgtaat	ccagcggact	360
cgttccaagc	ctgtgctcac	agggacacac	cctgtgaaca	caacgggtgg	cttcgggtgg	420
acaacgtcct	tccagtgcaa	ggtgcgcagt	gacgtgaagc	ctgtgatcca	gtggctgaag	480
cgggtggagt	acggctccga	gggacgccac	aactccacca	ttgatgtgg	tggccagaag	540
tttgtggtgt	tgcccacggg	tgatgtgtgg	tcacggcctg	atggctccta	cctcaacaag	600
ctgctcatct	ctcggggcccg	ccaggatgt	gctggcatgt	acatctgcct	aggtgcaaat	660
accatgggct	acagttccg	taggccttc	ctcactgtat	taccag		706

&lt;210&gt; 133

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Mouse

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&lt;400&gt; 133

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10				15			
Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
		20					25					30			
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu
				35			40				45				
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys
				50			55				60				
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys
		65			70			75				80			
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys
				85			90					95			
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr
				100			105					110			
Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly
				115			120				125				
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe
				130			135				140				
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys
		145			150			155				160			
Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
				165			170				175				
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
				180			185				190				
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln
				195			200				205				
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
				210			215				220				
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
				225			230				235				

&lt;210&gt; 134

&lt;211&gt; 340

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 134

atgacgcgga	cccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg			340

&lt;210&gt; 135

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 135

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10				15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
				20				25				30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
				35			40				45				
Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
				50			55				60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
				65			70				75			80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
				85			90				95				

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Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile  
 100 105 110  
 Met

<210> 136  
 <211> 148  
 <212> DNA  
 <213> Mouse

<400> 136  
 atgacgcgga gccccgcgt gctgctgctg ctattgggg ccctcccgtc ggctgaggcg 60  
 gcgcgagatg atattagtcc agggaaaggag agccctgggc caggtggttc ttcggggggc 120  
 caggaggacc cagccagcca gcagtggg 148

<210> 137  
 <211> 49  
 <212> PRT  
 <213> Mouse

<400> 137  
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro  
 1 5 10 15  
 Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro  
 20 25 30  
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln  
 35 40 45  
 Trp

<210> 138  
 <211> 352  
 <212> DNA  
 <213> Mouse

<400> 138  
 atgacgcgga gccccgcgt gctgctgctg ctattgggg ccctcccgtc ggctgaggcg 60  
 gcgcgagcac ggcctcgctt cacacagccc tccaaatgtg ggcgcgcgtt gattgcacgg 120  
 cctgtggta gctctgtgcg gctcaagtgt gtggccagt ggcacccacg gccagacatc 180  
 atgtggatga aggtgatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240  
 aagtggacac ttagctgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300  
 gtatctaaca aggccgggtgc catcaacgccc acctacaaag tggatgtaat cc 352

<210> 139  
 <211> 117  
 <212> PRT  
 <213> Mouse

<400> 139  
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro  
 1 5 10 15  
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys  
 20 25 30  
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu  
 35 40 45  
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys  
 50 55 60  
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys  
 65 70 75 80  
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys  
 85 90 95  
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr  
 100 105 110

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Lys Val Asp Val Ile  
115

<210> 140

<211> 421

<212> DNA

<213> Mouse

<400> 140

atgacgcgga	gccccgcgt	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagagc	ggactcggttc	caagcctgtg	ctcacagggg	cacaccctgt	gaacacaacg	120
gtggacttcg	gtgggacaac	gtccttccag	tgcaaggtgc	gcagtgcgt	gaagcctgtg	180
atccagtggc	tgaagcggt	ggagtaacggc	tccgagggac	gccacaactc	caccattgtat	240
gtgggtggcc	agaagttgt	gggtgtgccc	acgggtgtatg	tgtggtcacg	gcctgtatggc	300
tcctaccta	acaagctgct	catctctcg	gcccggcagg	atgatgctgg	catgtacatc	360
tgcctaggtg	caaataccat	gggctacagt	ttccgtacg	ctttcctcac	tgtattacca	420
g						421

<210> 141

<211> 140

<212> PRT

<213> Mouse

<400> 141

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1	5					10					15				
Ser	Ala	Glu	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr
		20				25					30				
Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser
		35				40					45				
Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu
	50						55				60				
Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp
	65		70		75		75			80					
Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser
					85		90			95					
Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg
		100				105		105			110				
Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
	115					120		120			125				
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro				
	130					135					140				

<210> 142

<211> 67

<212> DNA

<213> Mouse

<400> 142

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gcgcgag						67

<210> 143

<211> 22

<212> PRT

<213> Mouse

<400> 143

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1	5					10				15			
Ser	Ala	Glu	Ala	Ala	Arg								
		20											

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&lt;210&gt; 144

&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 1

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gcgcgaggac	ccccaa	aat ggcagacaaa	gtggtcccac	ggcagg	tgcc	120
cgcactgtgc	ggctacagt	cccagtgag	ggggacccac	caccgtt	gac catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgttcc	gtgtgt	ccagggtctg	240
aaggtaagg	aggtgaggc	cgaggatgcc	ggtgtt	tatg	tgtcaaggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatgtga	tgaaggatga	ccagac	360
acgcacatcg	aggctagtga	acacagaaag	aagaagtgg	ca	ctgagctt	420
aaggcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	480
gccacactaca	aagtggatgt	aatccagcg	actcg	ttcca	gc acagg	540
caccctgtga	acacaacggc	ggacttcg	gggacaacgt	ccttcc	caagg	600
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacgg	ctc cgagg	660
cacaactcca	ccattgatgt	gggtggccag	aagttgtgg	tgtgccc	ac ggtatgt	720
tggtcacggc	ctgatggctc	ctacctcaac	aagctgtca	tctctc	ggg cccaggat	780
gatgctggca	tgtacacctg	cctaggtgca	aataccatgg	gctacagtt	ccgtac	840
ttcctcactg	tattaccaga	ccccaaac	ccagg	cttc	atcg	900
tccacaagcc	tgccatggcc	tgtggtgatc	ggcatccc	ctgg	ccaggat	960
ggcactgtgc	tgctctggct	ttgcccagacc	aagaagaagc	catgt	gtatc	1020
cttcctgtgc	ctgggcatcg	tccccccaggg	acatccc	ccat	cgcc	1080
ctgccc	ctatgtgg	catatgtgag	gagcatgg	ccat	ccagg	1140
atcctggcct	ctggctcaac	tgctggccc	aagctgtacc	ccaagctata	cacagatgt	1200
cacacacaca	cacatacaca	cac	cacacgtct	catgtggagg	gcaagg	1260
tcaacaccag	catgtccact	atcagtgct	aatacagcga	atctcca	actgtgt	1320
gaggtaggca	tatggggcc	aaggcaacag	gttggagaa	ttgaga	acaa	1380
gtatcttag						1389

&lt;210&gt; 145

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 2

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
					20				25			30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
					35				40			45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
					50				55			60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					65				70			75			
Lys	Val	Lys	Glu	val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85				90			95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Met
					100				105			110			
Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His
					115				120			125			
Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp
					130				135			140			
Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn
					145				150			155			
Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val
					165				170			175			
Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr
					180				185			190			
Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln
					195				200			205			

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Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr  
210 215 220  
Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val  
225 230 235 240  
Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg  
245 250 255  
Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr  
260 265 270  
Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro  
275 280 285  
Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Thr Ser Leu  
290 295 300  
Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu  
305 310 315 320  
Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala  
325 330 335  
Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser  
340 345 350  
Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile  
355 360 365  
Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser  
370 375 380  
Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val  
385 390 395 400  
His Thr His Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly  
405 410 415  
Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr  
420 425 430  
Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg  
435 440 445  
Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser  
450 455 460